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(54) Title: NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE THEREOF

(57) Abstract: The invention provides nucleic acids containing single-nucleotide polymorphisms identified for transcribed human sequences, as well as methods of using the nucleic acids.

NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE THEREOF

BACKGROUND OF THE INVENTION

Sequence polymorphism-based analysis of nucleic acid sequences can augment or replace previously known methods for determining the identity and relatedness of individuals. The approach is generally based on alterations in nucleic acid sequences between related individuals. This analysis has been widely used in a variety of genetic, diagnostic, and forensic applications. For example, polymorphism analyses are used in identity and paternity analysis, and in genetic mapping studies.

One such type of variation is a restriction fragment length polymorphism (RFLP). RFLPS can create or delete a recognition sequence for a restriction endonuclease in one nucleic acid relative to a second nucleic acid. The result of the variation is an alteration in the relative length of restriction enzyme generated DNA fragments in the two nucleic acids.

Other polymorphisms take the form of short tandem repeats (STR) sequences, which are also referred to as variable numbers of tandem repeat (VNTR) sequences. STR sequences typically include tandem repeats of 2, 3, or 4 nucleotide sequences that are present in a nucleic acid from one individual but absent from a second, related individual at the corresponding genomic location.

Other polymorphisms take the form of single nucleotide variations, termed single nucleotide polymorphisms (SNPs), between individuals. A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA.

SNPs can arise in several ways. A single nucleotide polymorphism may arise due to a substitution of one nucleotide for another at the polymorphic site. Substitutions can be transitions or transversions. A transition is the replacement of one purine nucleotide by another purine nucleotide, or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine, or the converse.

Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Thus, the polymorphic site is a site at which one allele bears a gap with respect to a single nucleotide in another allele. Some SNPs occur within, or near genes. One such class includes SNPs falling within regions of genes

encoding for a polypeptide product. These SNPs may result in an alteration of the amino acid sequence of the polypeptide product and give rise to the expression of a defective or other variant protein. Such variant products can, in some cases result in a pathological condition, *e.g.*, genetic disease. Examples of genes in which a polymorphism within a coding sequence gives rise to genetic disease include sickle cell anemia and cystic fibrosis. Other SNPs do not result in alteration of the polypeptide product. Of course, SNPs can also occur in noncoding regions of genes.

SNPs tend to occur with great frequency and are spaced uniformly throughout the genome. The frequency and uniformity of SNPs means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest.

SUMMARY OF THE INVENTION

The invention is based in part on the discovery of novel single nucleotide polymorphisms (SNPs) in regions of human DNA.

Accordingly, in one aspect, the invention provides an isolated polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, *e.g.*, a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 7024) and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS: 1-7024), or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

The polynucleotide can be, *e.g.*, DNA or RNA, and can be between about 10 and about 100 nucleotides, *e.g.* 10-90, 10-75, 10-51, 10-40, or 10-30, nucleotides in length.

In some embodiments, the polymorphic site in the polymorphic sequence includes a nucleotide other than the nucleotide listed in Table 1, column 5 for the polymorphic sequence, *e.g.*, the polymorphic site includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

In other embodiments, the complement of the polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of

the polymorphic sequence, *e.g.*, the complement of the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

In some embodiments, the polymorphic sequence is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated with a polypeptide related to an ATPase associated protein, a cadherin, or any of the other proteins identified in Table 1, column 10.

In another aspect, the invention provides an isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 7024), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7024), provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

In some embodiments, the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide. The second polynucleotide can be, *e.g.*, (a) a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 7024), wherein the polymorphic sequence includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence; (b) a nucleotide sequence that is a fragment of any of the polymorphic sequences; (c) a complementary nucleotide sequence including a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7024), wherein the polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5; and (d) a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The invention also provides a method of detecting a polymorphic site in a nucleic acid. The method includes contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7024, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the nucleic acid and the oligonucleotide hybridize. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphic site in the nucleic acid.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

In some embodiments, the polymorphic sequence identified by the oligonucleotide is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated polypeptide related to an ATPase associated protein, cadherin, or any of the other protein families identified in Table 1, column 10.

In another aspect, the method includes determining if a sequence polymorphism is the present in a subject, such as a human. The method includes providing a nucleic acid from the subject and contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7024, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. Hybridization between the nucleic acid and the oligonucleotide is then determined. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphism in said subject.

In a further aspect, the invention provides a method of determining the relatedness of a first and second nucleic acid. The method includes providing a first nucleic acid and a second

nucleic acid and contacting the first nucleic acid and the second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7024, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the first nucleic acid and the second nucleic acid hybridize to the oligonucleotide, and comparing hybridization of the first and second nucleic acids to the oligonucleotide. Hybridization of first and second nucleic acids to the nucleic acid indicates the first and second subjects are related.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The method can be used in a variety of applications. For example, the first nucleic acid may be isolated from physical evidence gathered at a crime scene, and the second nucleic acid may be obtained from a person suspected of having committed the crime. Matching the two nucleic acids using the method can establish whether the physical evidence originated from the person.

In another example, the first sample may be from a human male suspected of being the father of a child and the second sample may be from the child. Establishing a match using the described method can establish whether the male is the father of the child.

In another aspect, the invention provides an isolated polypeptide comprising a polymorphic site at one or more amino acid residues, and wherein the protein is encoded by a polynucleotide including one of the polymorphic sequences SEQ ID NOS:1-7024, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

The polypeptide can be, *e.g.*, related to one of the protein families disclosed herein. For example, polypeptide can be related to an ATPase associated protein, cadherin, or any of the other proteins provided in Table 1, column 10.

In some embodiments, the polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.

In some embodiments, the polypeptide encoded by the polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.

The invention also provides an antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS:1-7024, or its complement. The polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

In some embodiments, the antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

Preferably, the antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence.

The invention further provides a method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject. The method includes providing a protein sample from the subject and contacting the sample with the above-described antibody under conditions that allow for the formation of antibody-antigen complexes. The antibody-antigen complexes are then detected. The presence of the complexes indicates the presence of the polypeptide.

The invention also provides a method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism

in a subject, *e.g.*, a human, non-human primate, cat, dog, rat, mouse, cow, pig, goat, or rabbit. The method includes providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or its complement, and treating the subject by administering to the subject an effective dose of a therapeutic agent. Aberrant expression can include qualitative alterations in expression of a gene, *e.g.*, expression of a gene encoding a polypeptide having an altered amino acid sequence with respect to its wild-type counterpart. Qualitatively different polypeptides can include, shorter, longer, or altered polypeptides relative to the amino acid sequence of the wild-type polypeptide. Aberrant expression can also include quantitative alterations in expression of a gene. Examples of quantitative alterations in gene expression include lower or higher levels of expression of the gene relative to its wild-type counterpart, or alterations in the temporal or tissue-specific expression pattern of a gene. Finally, aberrant expression may also include a combination of qualitative and quantitative alterations in gene expression.

The therapeutic agent can include, *e.g.*, second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele. In some embodiments, the second nucleic acid sequence comprises a polymorphic sequence which includes nucleotide listed in Table 1, column 5 for the polymorphic sequence.

Alternatively, the therapeutic agent can be a polypeptide encoded by a polynucleotide comprising polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7024, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

The therapeutic agent may further include an antibody as herein described, or an oligonucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7024, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for the polymorphic sequence.

In another aspect, the invention provides an oligonucleotide array comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed

therein. The first polynucleotide can be, e.g., a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 7024); a nucleotide sequence that is a fragment of any of the nucleotide sequences, provided that the fragment includes a polymorphic site in the polymorphic sequence; a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7024); or a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

In preferred embodiments, the array comprises 10; 100; 1,000; 10,000; 100,000 or more oligonucleotides.

The invention also provides a kit comprising one or more of the herein-described nucleic acids. The kit can include, e.g., a polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, e.g., a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 7024) and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS:1-7024), or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence. The invention provides an isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, e.g., a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 7024), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7024), provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention

belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides 3,404 distinct polymorphic sites (i.e., human cSNP's) based on genes that have not yet been previously identified. They are described in the Table included with this application for patent. The instant application presents only polymorphisms in nucleic acid sequences that have not previously been identified. For this reason, both nucleotide sequences for a reference-polymorphic pair are presented in the instant application. Since neither sequence was known prior to this invention, the choice of designating one sequence of the cognate pair as a "reference" sequence and the second cognate of the pair as a "polymorphic" sequence is arbitrary.

The SNPs are shown in Table 1 and the Sequence Listing. Both provide a summary of the polymorphic sequences disclosed herein. In the Table, a "SNP" is a polymorphic site embedded in a polymorphic sequence. The polymorphic site is occupied by a single nucleotide, which is the position of nucleotide variation between the wild type and polymorphic allelic sequences. The site is usually preceded by and followed by relatively highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations). Thus, a polymorphic sequence can include one or more of the following sequences: (1) a sequence having the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence; or (2) a sequence having a nucleotide other than the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence. An example of the latter sequence is a polymorphic sequence having the nucleotide denoted in Table 1, column 6 at the polymorphic site in the polymorphic sequence.

Nucleotide sequences for a referenced-polymorphic pair are presented in Table 1. Each cSNP entry provides information concerning the wild type nucleotide sequence as well as the corresponding sequence that includes the SNP at the polymorphic site. Since the wild type sequence is already known, the Sequence Listing accompanying this application provides only the sequence of the polymorphic allele; its SEQ ID NO: is also cross referenced in the Table 1. A reference to the SEQ ID NO: giving the translated amino acid sequence is also given if appropriate. The Table includes thirteen columns that provide descriptive information for each cSNP, each of which occupies one row in the Table. The column headings, and an explanation for each, are given below.

"SEQ ID" provides the cross-references to the two nucleotide SEQ ID NOs: for the cognate pair, which are numbered consecutively, and, as explained below, amino acid SEQ ID NOs: as well, in the Sequence Listing of the application. Conversely, each sequence entry in the Sequence Listing also includes a cross-reference to the CuraGen sequence ID, under the label "CuraGen sequence ID". The first pair of SEQ ID NOs: given in the first column of each row of the Table are the SEQ ID NOs: identifying the nucleic acid sequences for the polymorphisms. If a polymorphism carries an entry for the amino acid portion of the row, a third SEQ ID NO: appears in parentheses in the column "Amino acid before" (see below) for the reference amino acid sequence, and a fourth SEQ ID NO: appears in parentheses in the column "Amino acid after" (see below) for the polymorphic amino acid sequence. The latter SEQ ID NOs: refer to amino acid sequences giving the cognate reference and polymorphic amino acid sequences that are the translation of the nucleotide polymorphism. If a polymorphism carries no entry for the protein portion of the row, only one pair SEQ ID NOs: is provided, in the first column.

"Base pos. of SNP" gives the numerical position of the nucleotide in the nucleic acid at which the cSNP is found, as identified in this invention.

"Polymorphic sequence" provides a 51-base sequence with the polymorphic site at the 26th base in the sequence, as well as 25 bases from the reference sequence on the 5' side and the 3' side of the polymorphic site. The designation at the polymorphic site is enclosed in square brackets, and provides first, the reference nucleotide; second, a "slash (/)"; and third, the polymorphic nucleotide. In certain cases the polymorphism is an insertion or a deletion. In that case, the position which is "unfilled" (i.e., the reference or the polymorphic position) is indicated by the word "gap".

“Base before” provides the nucleotide present in the reference sequence at the position at which the polymorphism is found.

“Base after” provides the altered nucleotide at the position of the polymorphism.

“Amino acid before” provides the amino acid in the reference protein, if the polymorphism occurs in a coding region. This column also includes the SEQ ID NO: in parentheses for the translated reference amino acid sequence if the polymorphism occurs in a coding region.

“Amino acid after” provides the amino acid in the polymorphic protein, if the polymorphism occurs in a coding region. This column also includes the SEQ ID NO: in parentheses for the translated polymorphic amino acid sequence if the polymorphism occurs in a coding region.

“Type of change” provides information on the nature of the polymorphism.

“SILENT-NONCODING” is used if the polymorphism occurs in a noncoding region of a nucleic acid.

“SILENT-CODING” is used if the polymorphism occurs in a coding region of a nucleic acid and results in no change of amino acid in the translated polymorphic protein.

“CONSERVATIVE” is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in the same class as the reference amino acid. The classes are:

Aliphatic: Gly, Ala, Val, Leu, Ile;

Aromatic: Phe, Tyr, Trp;

Sulfur-containing: Cys, Met;

Aliphatic OH: Ser, Thr;

Basic: Lys, Arg, His;

Acidic: Asp, Glu, Asn, Gln;

Pro falls in none of the other classes; and

End defines a termination codon.

“NONCONSERVATIVE” is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in a different class than the reference amino acid.

“FRAMESHIFT” relates to an insertion or a deletion. If the frameshift occurs in a coding region, the Table provides the translation of the frameshifted codons 3' to the polymorphic site.

“Protein classification of CuraGen gene” provides a generic class into which the protein is classified. During the course of the work leading to the filing of the four applications identified above, approximately 100 classes of proteins were identified. They are described further below.

“Name of protein identified following a BLASTX analysis of the CuraGen sequence” provides the database reference for the protein found to resemble the novel reference-polymorphism cognate pair most closely. (The next paragraph explains how a sequence was determined to be “novel”).

“Similarity (pvalue) following a BLASTX analysis” provides the pvalue, a statistical measure from the BLASTX analysis that the polymorphic sequence is similar to, and therefore an allele of, the reference, or wild-type, sequence. In the present application, a cutoff of $pvalue > 1 \times 10^{-50}$ (entered, for example, as 1.0E-50 in the Table) is used to establish that the reference-polymorphic cognate pairs are novel.

“Map location” provides any information available at the time of filing related to localization of a gene on a chromosome.

The polymorphisms are arranged in the Table in the following order.

SEQ ID NOs: 1-6592, in consecutive pairs, are SNPs that are silent.

SEQ ID NOs: 6593-6648, in consecutive pairs, are SNPs that lead to conservative amino acid changes.

SEQ ID NOs: 6649-7024, in consecutive pairs, are SNPs that lead to nonconservative amino acid changes.

SEQ ID NOs: 6809-6864, in consecutive pairs, are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to conservative amino acid changes between the reference and the polymorphic sequences. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 44335-44850, as described in U.S.S.N. 60/168,138, filed November 30, 1999. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

SEQ ID NOs: 6865-7024, in consecutive pairs, are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to nonconservative amino acid changes between the reference and the polymorphic sequences. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 44851-46464, as described in U.S.S.N. 60/168,138, filed November 30, 1999. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

Provided herein are compositions which include, or are capable of detecting, nucleic acid sequences having these polymorphisms, as well as methods of using nucleic acids.

IDENTIFICATION OF INDIVIDUALS CARRYING SNPs

Individuals carrying polymorphic alleles of the invention may be detected at either the DNA, the RNA, or the protein level using a variety of techniques that are well known in the art. Strategies for identification and detection are described in *e.g.*, EP 730,663, EP 717,113, and PCT US97/02102. The present methods usually employ pre-characterized polymorphisms. That is, the genotyping location and nature of polymorphic forms present at a site have already been determined. The availability of this information allows sets of probes to be designed for specific identification of the known polymorphic forms.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by *e.g.*, PCR. See generally PCR Technology: Principles and Applications for DNA Amplification (ed. H.A. Erlich, Freeman Press, NY, NY, 1992);

PCR Protocols: A Guide to Methods and Applications (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., Nucleic Acids Res. 19, 4967 (1991); Eckert et al., PCR Methods and Applications 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

The phrase "recombinant protein" or "recombinantly produced protein" refers to a peptide or protein produced using non-native cells that do not have an endogenous copy of DNA able to express the protein. In particular, as used herein, a recombinantly produced protein relates to the gene product of a polymorphic allele, i.e., a "polymorphic protein" containing an altered amino acid at the site of translation of the nucleotide polymorphism. The cells produce the protein because they have been genetically altered by the introduction of the appropriate nucleic acid sequence. The recombinant protein will not be found in association with proteins and other subcellular components normally associated with the cells producing the protein. The terms "protein" and "polypeptide" are used interchangeably herein.

The phrase "substantially purified" or "isolated" when referring to a nucleic acid, peptide or protein, means that the chemical composition is in a milieu containing fewer, or preferably, essentially none, of other cellular components with which it is naturally associated. Thus, the phrase "isolated" or "substantially pure" refers to nucleic acid preparations that lack at least one protein or nucleic acid normally associated with the nucleic acid in a host cell. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as gel electrophoresis or high performance liquid chromatography. Generally, a substantially purified or isolated nucleic acid or protein will comprise more than 80% of all macromolecular species present in the preparation. Preferably, the nucleic acid or protein is purified to represent greater than 90% of all macromolecular species present. More preferably the nucleic acid or protein is purified to greater than 95%, and most preferably the nucleic acid or protein is purified to essential homogeneity, wherein other macromolecular species are not detected by conventional analytical procedures.

The genomic DNA used for the diagnosis may be obtained from any nucleated cells of the body, such as those present in peripheral blood, urine, saliva, buccal samples, surgical specimen, and autopsy specimens. The DNA may be used directly or may be amplified enzymatically in vitro through use of PCR (Saiki et al. Science 239:487-491 (1988)) or other in vitro amplification methods such as the ligase chain reaction (LCR) (Wu and Wallace

Genomics 4:560-569 (1989)), strand displacement amplification (SDA) (Walker et al. Proc. Natl. Acad. Sci. U.S.A. 89:392-396 (1992)), self-sustained sequence replication (3SR) (Fahy et al. PCR Methods P&J 1:25-33 (1992)), prior to mutation analysis.

The method for preparing nucleic acids in a form that is suitable for mutation detection is well known in the art. A "nucleic acid" is a deoxyribonucleotide or ribonucleotide polymer in either single- or double-stranded form, including known analogs of natural nucleotides unless otherwise indicated. The term "nucleic acids", as used herein, refers to either DNA or RNA. "Nucleic acid sequence" or "polynucleotide sequence" refers to a single-stranded sequence of deoxyribonucleotide or ribonucleotide bases read from the 5' end to the 3' end. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 5' end of the RNA transcript in the 5' direction are referred to as "upstream sequences"; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 3' end of the RNA transcript in the 3' direction are referred to as "downstream sequences". The term includes both self-replicating plasmids, infectious polymers of DNA or RNA and nonfunctional DNA or RNA. The complement of any nucleic acid sequence of the invention is understood to be included in the definition of that sequence. "Nucleic acid probes" may be DNA or RNA fragments.

The detection of polymorphisms in specific DNA sequences, can be accomplished by a variety of methods including, but not limited to, restriction-fragment-length-polymorphism detection based on allele-specific restriction-endonuclease cleavage (Kan and Dozy Lancet ii:910-912 (1978)), hybridization with allele-specific oligonucleotide probes (Wallace et al. Nucl. Acids Res. 6:3543-3557 (1978)), including immobilized oligonucleotides (Saiki et al. Proc. Natl. Acad. Sci. USA, 86:6230-6234 (1969)) or oligonucleotide arrays (Maskos and Southern Nucl. Acids Res 21:2269-2270 (1993)), allele-specific PCR (Newton et al. Nucl Acids Res 17:2503-2516 (1989)), mismatch-repair detection (MRD) (Faham and Cox Genome Res 5:474-482 (1995)), binding of MutS protein (Wagner et al. Nucl Acids Res 23:3944-3948 (1995)), denaturing-gradient gel electrophoresis (DGGE) (Fisher and Lerman et al. Proc. Natl. Acad. Sci. U.S.A. 80:1579-1583 (1983)), single-strand-conformation-polymorphism detection (Orita et al. Genomics 5:874-879 (1983)), RNAase cleavage at mismatched base-pairs (Myers et al. Science 230:1242 (1985)), chemical (Cotton et al. Proc. Natl. w Sci. U.S.A., 8Z4397-4401 (1988)) or enzymatic (Youil et al. Proc. Natl. Acad. Sci. U.S.A. 92:87-91 (1995)) cleavage of heteroduplex DNA, methods based on allele specific

primer extension (Syvanen et al. Genomics 8:684-692 (1990)), genetic bit analysis (GBA) (Nikiforov et al. &&I Acids 22:4167-4175 (1994)), the oligonucleotide-ligation assay (OLA) (Landegren et al. Science 241:1077 (1988)), the allele-specific ligation chain reaction (LCR) (Barrany Proc. Natl. Acad. Sci. U.S.A. 88:189-193 (1991)), gap-LCR (Abravaya et al. Nucl Acids Res 23:675-682 (1995)), radioactive and/or fluorescent DNA sequencing using standard procedures well known in the art, and peptide nucleic acid (PNA) assays (Orum et al., Nucl. Acids Res, 21:5332-5356 (1993); Thiede et al., Nucl. Acids Res. 24:983-984 (1996)).

“Specific hybridization” or “selective hybridization” refers to the binding, or duplexing, of a nucleic acid molecule only to a second particular nucleotide sequence to which the nucleic acid is complementary, under suitably stringent conditions when that sequence is present in a complex mixture (e.g., total cellular DNA or RNA). “Stringent conditions” are conditions under which a probe will hybridize to its target subsequence, but to no other sequences. Stringent conditions are sequence-dependent and are different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter ones. Generally, stringent conditions are selected such that the temperature is about 5°C lower than the thermal melting point (T_m) for the specific sequence to which hybridization is intended to occur at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% of the target sequence hybridizes to the complementary probe at equilibrium. Typically, stringent conditions include a salt concentration of at least about 0.01 to about 1.0 M Na ion concentration (or other salts), at pH 7.0 to 8.3. The temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides). Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C are suitable for allele-specific probe hybridization.

“Complementary” or “target” nucleic acid sequences refer to those nucleic acid sequences which selectively hybridize to a nucleic acid probe. Proper annealing conditions depend, for example, upon a probe’s length, base composition, and the number of mismatches and their position on the probe, and must often be determined empirically. For discussions of nucleic acid probe design and annealing conditions, see, for example, Sambrook et al., or Current Protocols in Molecular Biology, F. Ausubel *et al.*, ed., Greene Publishing and Wiley-Interscience, New York (1987).

A perfectly matched probe has a sequence perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion of the target sequence. A "polymorphic" marker or site is the locus at which a sequence difference occurs with respect to a reference sequence. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats, and insertion elements such as Alu. The reference allelic form may be, for example, the most abundant form in a population, or the first allelic form to be identified, and other allelic forms are designated as alternative, variant or polymorphic alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the "wild type" form, and herein may also be referred to as the "reference" form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has two distinguishable forms (i.e., base sequences), and a triallelic polymorphism has three such forms.

As used herein an "oligonucleotide" is a single-stranded nucleic acid ranging in length from 2 to about 60 bases. Oligonucleotides are often synthetic but can also be produced from naturally occurring polynucleotides. A probe is an oligonucleotide capable of binding to a target nucleic acid of a complementary sequence through one or more types of chemical bonds, usually through complementary base pairing via hydrogen bond formation. Oligonucleotide probes are often between 5 and 60 bases, and, in specific embodiments, may be between 10-40, or 15-30 bases long. An oligonucleotide probe may include natural (i.e. A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in an oligonucleotide probe may be joined by a linkage other than a phosphodiester bond, such as a phosphoramidite linkage or a phosphorothioate linkage, or they may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than by phosphodiester bonds, so long as it does not interfere with hybridization.

As used herein, the term "primer" refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and a polymerization agent, such as DNA polymerase, RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the

template. A primer need not be perfectly complementary to the exact sequence of the template, but should be sufficiently complementary to hybridize with it. The term "primer site" refers to the sequence of the target DNA to which a primer hybridizes. The term "primer pair" refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

DNA fragments can be prepared, for example, by digesting plasmid DNA, or by use of PCR. Oligonucleotides for use as primers or probes are chemically synthesized by methods known in the field of the chemical synthesis of polynucleotides, including by way of non-limiting example the phosphoramidite method described by Beaucage and Carruthers, Tetrahedron Lett 22:1859-1862 (1981) and the triester method provided by Matteucci, et al., J. Am. Chem. Soc., 103:3185 (1981) both incorporated herein by reference. These syntheses may employ an automated synthesizer, as described in Needham-VanDevanter, D.R., et al., Nucleic Acids Res. 12:61596168 (1984). Purification of oligonucleotides may be carried out by either native acrylamide gel electrophoresis or by anion-exchange HPLC as described in Pearson, J.D. and Regnier, F.E., J. Chrom., 255:137-149 (1983). A double stranded fragment may then be obtained, if desired, by annealing appropriate complementary single strands together under suitable conditions or by synthesizing the complementary strand using a DNA polymerase with an appropriate primer sequence. Where a specific sequence for a nucleic acid probe is given, it is understood that the complementary strand is also identified and included. The complementary strand will work equally well in situations where the target is a double-stranded nucleic acid.

The sequence of the synthetic oligonucleotide or of any nucleic acid fragment can be obtained using either the dideoxy chain termination method or the Maxam-Gilbert method (see Sambrook et al. Molecular Cloning - a Laboratory Manual (2nd Ed.), Vols. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1989), which is incorporated herein by reference. This manual is hereinafter referred to as "Sambrook et al."; Zyskind et al., (1988)). Recombinant DNA Laboratory Manual, (Acad. Press, New York). Oligonucleotides useful in diagnostic assays are typically at least 8 consecutive nucleotides in length, and may range upwards of 18 nucleotides in length to greater than 100 or more consecutive nucleotides.

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the SNP-

containing nucleotide sequences of the invention, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, about 25, about 50, or about 60 nucleotides or an entire SNP coding strand, or to only a portion thereof.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a polymorphic nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. For example, the antisense nucleic acid molecule can generally be complementary to the entire coding region of an mRNA, but more preferably as embodied herein, it is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of the mRNA. An antisense oligonucleotide can range in length between about 5 and about 60 nucleotides, preferably between about 10 and about 45 nucleotides, more preferably between about 15 and 40 nucleotides, and still more preferably between about 15 and 30 in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-

2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following section).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a polymorphic protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementary to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The

antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: "reference sequence", "comparison window", "sequence identity", "percentage of sequence identity", and "substantial identity". A "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing, or may comprise a complete cDNA or gene sequence. Optimal alignment of sequences for aligning a comparison window may, for example, be conducted by the local homology algorithm of Smith and Waterman Adv. Appl. Math. 2482 (1981), by the homology alignment algorithm of Needleman and Wunsch J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson and Lipman Proc. Natl. Acad. Sci. U.S.A. 852444 (1988), or by computerized implementations of these algorithms (for example, GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, WI).

Techniques for nucleic acid manipulation of the nucleic acid sequences harboring the cSNP's of the invention, such as subcloning nucleic acid sequences encoding polypeptides into expression vectors, labeling probes, DNA hybridization, and the like, are described generally in Sambrook *et al.*, The phrase "nucleic acid sequence encoding" refers to a nucleic acid which directs the expression of a specific protein, peptide or amino acid sequence. The nucleic acid sequences include both the DNA strand sequence that is transcribed into RNA and the RNA sequence that is translated into protein, peptide or amino acid sequence. The nucleic acid sequences include both the full length nucleic acid sequences disclosed herein as well as non-full length sequences derived from the full length protein. It being further understood that the sequence includes the degenerate codons of the native sequence or sequences which may be introduced to provide codon preference in a specific host cell. Consequently, the principles of probe selection and array design can readily be extended to analyze more complex polymorphisms (see EP 730,663). For example, to characterize a triallelic SNP polymorphism, three groups of probes can be designed tiled on the three polymorphic forms as described above. As a further example, to analyze a diallelic polymorphism involving a deletion of a nucleotide, one can tile a first group of probes based

on the undeleted polymorphic form as the reference sequence and a second group of probes based on the deleted form as the reference sequence.

For assays of genomic DNA, virtually any biological convenient tissue sample can be used. Suitable samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. Genomic DNA is typically amplified before analysis. Amplification is usually effected by PCR using primers flanking a suitable fragment e.g., of 50-500 nucleotides containing the locus of the polymorphism to be analyzed. Target is usually labeled in the course of amplification. The amplification product can be RNA or DNA, single stranded or double stranded. If double stranded, the amplification product is typically denatured before application to an array. If genomic DNA is analyzed without amplification, it may be desirable to remove RNA from the sample before applying it to the array. Such can be accomplished by digestion with DNase-free RNase.

DETECTION OF POLYMORPHISMS IN A NUCLEIC ACID SAMPLE

The SNPs disclosed herein can be used to determine which forms of a characterized polymorphism are present in individuals under analysis.

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 7, 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in published PCT application WO 95/11995. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

An allele-specific primer hybridizes to a site on a target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17 2427-2448 (1989). This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co New York, 1992, Chapter 7).

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base

sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

The genotype of an individual with respect to a pathology suspected of being caused by a genetic polymorphism may be assessed by association analysis. Phenotypic traits suitable for association analysis include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria).

Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, oral cavity, ovary, pancreas, prostate, skin, stomach, leukemia, liver, lung, and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). Since the polymorphic sites are within a 50,000 bp region in the human genome, the probability of recombination between these polymorphic sites is low. That low probability means the haplotype (the set of all 10 polymorphic sites) set forth in this application should be inherited without change for at least several generations. The more sites that are analyzed the lower the probability that the set of polymorphic forms in one individual is the same as that in an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are diallelic because the population frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic

loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a match of suspect and crime scene sample would occur by chance.

$p(ID)$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In diallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism are (see WO 95/12607):

$$\text{Homozygote: } p(AA)=x^2$$

$$\text{Homozygote: } p(BB)=y^2=(1-x)^2$$

$$\text{Single Heterozygote: } p(AB)=p(BA)=xy=x(1-x)$$

$$\text{Both Heterozygotes: } p(AB+BA)=2xy=2x(1-x)$$

The probability of identity at one locus (i.e, the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID)=(x^2)^2+(2xy)^2+(y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

$$p(ID)=x^{4+} (2xy)^{2+} (2yz)^{2+} (2xz)^{2+} z^{4+} y^4$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

The cumulative probability of identity ($cum\ p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus:

$$cum\ p(ID)=p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$cum\ p(nonID)=1-cum\ p(ID).$$

If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

If the set of polymorphisms in the child attributable to the father does not match the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him incompatible as the father) is given by the equation (see WO 95/12607):

$$p(exc)=xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a diallelic polymorphic site.

(At a triallelic site $p(exc) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x , y and z and the respective population frequencies of alleles A, B and C). The probability of non-exclusion is:

$$p(non-exc) = 1 - p(exc)$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$cum\ p(non-exc) = p(non-exc1)p(non-exc2)p(non-exc3) \dots p(non-excn)$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded) is:

$$cum\ p(exc) = 1 - cum\ p(non-exc).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components. Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus

erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic marker sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the individuals, some of whom exhibit a particular trait, and some of whom exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., U.S. Pat. No. 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wild type with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered.

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992) (each of which is incorporated by reference in its entirety for all purposes).

Linkage studies are typically performed on members of a family. Available members of the family are characterized for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction RF , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (RF), ranging

from $RF=0.0$ (coincident loci) to $RF=0.50$ (unlinked). Thus, the likelihood at a given value of RF is: probability of data if loci linked at RF to probability of data if loci unlinked. The computed likelihood is usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of RF (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of RF at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of RF) than the possibility that the two loci are unlinked. By convention, a combined lod score of + 3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. (1989). Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292. The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

The invention further provides methods for assessing the pharmacogenomic susceptibility of a subject harboring a single nucleotide polymorphism to a particular

pharmaceutical compound, or to a class of such compounds. Genetic polymorphism in drug-metabolizing enzymes, drug transporters, receptors for pharmaceutical agents, and other drug targets have been correlated with individual differences based on distinction in the efficacy and toxicity of the pharmaceutical agent administered to a subject. Pharmacogenomic characterization of a subjects susceptibility to a drug enhances the ability to tailor a dosing regimen to the particular genetic constitution of the subject, thereby enhancing and optimizing the therapeutic effectiveness of the therapy.

In cases in which a cSNP leads to a polymorphic protein that is ascribed to be the cause of a pathological condition, method of treating such a condition includes administering to a subject experiencing the pathology the wild type cognate of the polymorphic protein. Once administered in an effective dosing regimen, the wild type cognate provides complementation or remediation of the defect due to the polymorphic protein. The subject's condition is ameliorated by this protein therapy.

A subject suspected of suffering from a pathology ascribable to a polymorphic protein that arises from a cSNP is to be diagnosed using any of a variety of diagnostic methods capable of identifying the presence of the cSNP in the nucleic acid, or of the cognate polymorphic protein, in a suitable clinical sample taken from the subject. Once the presence of the cSNP has been ascertained, and the pathology is correctable by administering a normal or wild-type gene, the subject is treated with a pharmaceutical composition that includes a nucleic acid that harbors the correcting wild-type gene, or a fragment containing a correcting sequence of the wild-type gene. Non-limiting examples of ways in which such a nucleic acid may be administered include incorporating the wild-type gene in a viral vector, such as an adenovirus or adeno associated virus, and administration of a naked DNA in a pharmaceutical composition that promotes intracellular uptake of the administered nucleic acid. Once the nucleic acid that includes the gene coding for the wild-type allele of the polymorphism is incorporated within a cell of the subject, it will initiate *de novo* biosynthesis of the wild-type gene product. If the nucleic acid is further incorporated into the genome of the subject, the treatment will have long-term effects, providing *de novo* synthesis of the wild-type protein for a prolonged duration. The synthesis of the wild-type protein in the cells of the subject will contribute to a therapeutic enhancement of the clinical condition of the subject.

A subject suffering from a pathology ascribed to a SNP may be treated so as to correct the genetic defect. (See Kren et al., Proc. Natl. Acad. Sci. USA 96:10349-10354 (1999)). Such a subject is identified by any method that can detect the polymorphism in a sample

drawn from the subject. Such a genetic defect may be permanently corrected by administering to such a subject a nucleic acid fragment incorporating a repair sequence that supplies the wild-type nucleotide at the position of the SNP. This site-specific repair sequence encompasses an RNA/DNA oligonucleotide which operates to promote endogenous repair of a subject's genomic DNA. Upon administration in an appropriate vehicle, such as a complex with polyethylenimine or encapsulated in anionic liposomes, a genetic defect leading to an inborn pathology may be overcome, as the chimeric oligonucleotides induces incorporation of the wild-type sequence into the subject's genome. Upon incorporation, the wild-type gene product is expressed, and the replacement is propagated, thereby engendering a permanent repair.

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10, 100, 1000 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the hybridizing methods.

Several aspects of the present invention rely on having available the polymorphic proteins encoded by the nucleic acids comprising a SNP of the inventions. There are various methods of isolating these nucleic acid sequences. For example, DNA is isolated from a genomic or cDNA library using labeled oligonucleotide probes having sequences complementary to the sequences disclosed herein.

Such probes can be used directly in hybridization assays. Alternatively probes can be designed for use in amplification techniques such as PCR.

To prepare a cDNA library, mRNA is isolated from tissue such as heart or pancreas, preferably a tissue wherein expression of the gene or gene family is likely to occur. cDNA is prepared from the mRNA and ligated into a recombinant vector. The vector is transfected into a recombinant host for propagation, screening and cloning. Methods for making and screening

cDNA libraries are well known, See Gubler, U. and Hoffman, B.J. *Gene* 25:263-269 (1983) and Sambrook et al.

For a genomic library, for example, the DNA is extracted from tissue and either mechanically sheared or enzymatically digested to yield fragments of about 12-20 kb. The fragments are then separated by gradient centrifugation from undesired sizes and are constructed in bacteriophage lambda vectors. These vectors and phage are packaged *in vitro*, as described in Sambrook, et al. Recombinant phage are analyzed by plaque hybridization as described in Benton and Davis, *Science* 196:180-182 (1977). Colony hybridization is carried out as generally described in M. Grunstein et al. *Proc. Natl. Acad. Sci. USA*. 72:3961-3965 (1975). DNA of interest is identified in either cDNA or genomic libraries by its ability to hybridize with nucleic acid probes, for example on Southern blots, and these DNA regions are isolated by standard methods familiar to those of skill in the art. See Sambrook, et al.

In PCR techniques, oligonucleotide primers complementary to the two 3' borders of the DNA region to be amplified are synthesized. The polymerase chain reaction is then carried out using the two primers. See PCR Protocols: a Guide to Methods and Applications (Innis, M, Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990). Primers can be selected to amplify the entire regions encoding a full-length sequence of interest or to amplify smaller DNA segments as desired. PCR can be used in a variety of protocols to isolate cDNAs encoding a sequence of interest. In these protocols, appropriate primers and probes for amplifying DNA encoding a sequence of interest are generated from analysis of the DNA sequences listed herein. Once such regions are PCR-amplified, they can be sequenced and oligonucleotide probes can be prepared from the sequence.

Once DNA encoding a sequence comprising a cSNP is isolated and cloned, one can express the encoded polymorphic proteins in a variety of recombinantly engineered cells. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of DNA encoding a sequence of interest. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes is made here.

In brief summary, the expression of natural or synthetic nucleic acids encoding a sequence of interest will typically be achieved by operably linking the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either

prokaryotes or eukaryotes. Typical expression vectors contain initiation sequences, transcription and translation terminators, and promoters useful for regulation of the expression of a polynucleotide sequence of interest. To obtain high level expression of a cloned gene, it is desirable to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. The expression vectors may also comprise generic expression cassettes containing at least one independent terminator sequence, sequences permitting replication of the plasmid in both eukaryotes and prokaryotes, i.e., shuttle vectors, and selection markers for both prokaryotic and eukaryotic systems. See Sambrook et al.

A variety of prokaryotic expression systems may be used to express the polymorphic proteins of the invention. Examples include *E. coli*, *Bacillus*, *Streptomyces*, and the like.

It is preferred to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. Examples of regulatory regions suitable for this purpose in *E. coli* are the promoter and operator region of the *E. coli* tryptophan biosynthetic pathway as described by Yanofsky, C., J. *Bacterial*. 158:1018-1024 (1984) and the leftward promoter of phage lambda as described by A, I. and Hagen, D., Ann. Rev. Genet. 14:399-445 (1980). The inclusion of selection markers in DNA vectors transformed in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin, tetracycline, or chloramphenicol. See Sambrook et al. for details concerning selection markers for use in *E. coli*.

To enhance proper folding of the expressed recombinant protein, during purification from *E. coli*, the expressed protein may first be denatured and then renatured. This can be accomplished by solubilizing the bacterially produced proteins in a chaotropic agent such as guanidine HCl and reducing all the cysteine residues with a reducing agent such as beta-mercaptoethanol. The protein is then renatured, either by slow dialysis or by gel filtration. See U.S. Patent No. 4,511,503. Detection of the expressed antigen is achieved by methods known in the art as radioimmunoassay, or Western blotting techniques or immunoprecipitation. Purification from *E. coli* can be achieved following procedures such as those described in U.S. Patent No. 4,511,503.

Any of a variety of eukaryotic expression systems such as yeast, insect cell lines, bird, fish, and mammalian cells, may also be used to express a polymorphic protein of the

invention. As explained briefly below, a nucleotide sequence harboring a cSNP may be expressed in these eukaryotic systems. Synthesis of heterologous proteins in yeast is well known. Methods in Yeast Genetics, Sherman, F., et al., Cold Spring Harbor Laboratory, (1982) is a well recognized work describing the various methods available to produce the protein in yeast. Suitable vectors usually have expression control sequences, such as promoters, including 3-phosphoglycerate kinase or other glycolytic enzymes, and an origin of replication, termination sequences and the like as desired. For instance, suitable vectors are described in the literature (Botstein, et al., *Gene* 8:17-24 (1979); Broach, et al., *Gene* 8:121-133 (1979)).

Two procedures are used in transforming yeast cells. In one case, yeast cells are first converted into protoplasts using zymolyase, lyticase or glucanase, followed by addition of DNA and polyethylene glycol (PEG). The PEG-treated protoplasts are then regenerated in a 3% agar medium under selective conditions. Details of this procedure are given in the papers by J.D. Beggs, *Nature* (London) 275:104-109 (1978); and Hinnen, A., et al., *Proc. Natl. Acad. Sci. USA*, 75:1929-1933 (1978). The second procedure does not involve removal of the cell wall. Instead the cells are treated with lithium chloride or acetate and PEG and put on selective plates (Ito, H., et al., *J. Bact.*, 153:163-168 (1983)) cells and applying standard protein isolation techniques to the lysates.

The purification process can be monitored by using Western blot techniques or radioimmunoassay or other standard techniques. The sequences encoding the proteins of the invention can also be ligated to various immunoassay expression vectors for use in transforming cell cultures of, for instance, mammalian, insect, bird or fish origin. Illustrative of cell cultures useful for the production of the polypeptides are mammalian cells. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host cell lines capable of expressing intact proteins have been developed in the art, and include the HEK293, BHK21, and CHO cell lines, and various human cells such as COS cell lines, HeLa cells, myeloma cell lines, Jurkat cells, etc. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter (e.g., the CMV promoter, a HSV *tk* promoter or *pgk* (phosphoglycerate kinase) promoter), an enhancer (Queen et al. *Immunol. Rev.* 89:49 (1986)) and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (e.g., an SV40 large T Ag poly A addition site), and transcriptional terminator sequences.

Other animal cells are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7th edition, (1992)). Appropriate vectors for expressing the proteins of the invention in insect cells are usually derived from baculovirus. Insect cell lines include mosquito larvae, silkworm, armyworm, moth and *Drosophila* cell lines such as a Schneider cell line (See Schneider J. Embryol. Exp. Morphol., 27:353-365 (1987)). As indicated above, the vector, e.g., a plasmid, which is used to transform the host cell, preferably contains DNA sequences to initiate transcription and sequences to control the translation of the protein. These sequences are referred to as expression control sequences. As with yeast, when higher animal host cells are employed, polyadenylation or transcription terminator sequences from known mammalian genes need to be incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also be included. An example of a splicing sequence is the VP1 intron from SV40 (Sprague, J. et al., J. Virol. 45: 773-781 (1983)). Additionally, gene sequences to control replication in the host cell may be Saveria-Campo, M., 1985, "Bovine Papilloma virus DNA a Eukaryotic Cloning Vector" in DNA Cloning Vol. II a Practical Approach Ed. D.M. Glover, IRL Press, Arlington, Virginia pp. 213-238. The host cells are competent or rendered competent for transformation by various means. There are several well-known methods of introducing DNA into animal cells. These include: calcium phosphate precipitation, fusion of the recipient cells with bacterial protoplasts containing the DNA, treatment of the recipient cells with liposomes containing the DNA, DEAE dextran, electroporation and micro-injection of the DNA directly into the cells.

The transformed cells are cultured by means well known in the art (Biochemical Methods in Cell Culture and Virology, Kuchler, R.J., Dowden, Hutchinson and Ross, Inc., (1977)). The expressed polypeptides are isolated from cells grown as suspensions or as monolayers. The latter are recovered by well known mechanical, chemical or enzymatic means.

General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" refers to linkage of a promoter upstream from a DNA sequence such that the promoter mediates transcription of the DNA sequence. Specifically, "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the gene encoding the protein is expressed

by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression sequence. The term "vector", refers to viral expression systems, autonomous self-replicating circular DNA (plasmids), and includes both expression and nonexpression plasmids.

The term "gene" as used herein is intended to refer to a nucleic acid sequence which encodes a polypeptide. This definition includes various sequence polymorphisms, mutations, and/or sequence variants wherein such alterations do not affect the function of the gene product. The term "gene" is intended to include not only coding sequences but also regulatory regions such as promoters, enhancers, termination regions and similar untranslated nucleotide sequences. The term further includes all introns and other DNA sequences spliced from the mRNA transcript, along with variants resulting from alternative splice sites.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A43 1 cells, human Co10205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL- 60, U937, HaK or Jurkat cells. Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida* or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac© kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed." The protein of the invention may

be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein.

The polymorphic protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein. The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art.

The polymorphic proteins produced by recombinant DNA technology may be purified by techniques commonly employed to isolate or purify recombinant proteins. Recombinantly produced proteins can be directly expressed or expressed as a fusion protein. The protein is then purified by a combination of cell lysis (e.g., sonication) and affinity chromatography. For fusion products, subsequent digestion of the fusion protein with an appropriate proteolytic enzyme releases the desired polypeptide. The polypeptides of this invention may be purified to substantial purity by standard techniques well known in the art, including selective precipitation with such substances as ammonium sulfate, column chromatography, immunopurification methods, and others. See, for instance, R. Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag: New York (1982), incorporated herein by reference. For example, in an embodiment, antibodies may be raised to the proteins of the invention as described herein. Cell membranes are isolated from a cell line expressing the recombinant protein, the protein is extracted from the membranes and immunoprecipitated. The proteins may then be further purified by standard protein chemistry techniques as described above.

The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-Toyopearl® or Cibacrom blue 3GA Sepharose B; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography. Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New

England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT). Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as polymorphic. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human polymorphic proteins are disclosed.

The phrase "specifically binds to", "immunospecifically binds to" or is "specifically immunoreactive with", an antibody when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biological materials. Thus, for example, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. Of particular interest in the present invention is an antibody that binds immunospecifically to a polymorphic protein but not to its cognate wild type allelic protein, or vice versa. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) *Antibodies, a Laboratory Manual*, Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

Polyclonal and/or monoclonal antibodies that immunospecifically bind to polymorphic gene products but not to the corresponding prototypical or "wild-type" gene

products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product.

An isolated polymorphic protein, or a portion or fragment thereof, can be used as an immunogen to generate the antibody that binds the polymorphic protein using standard techniques for polyclonal and monoclonal antibody preparation. The full-length polymorphic protein can be used or, alternatively, the invention provides antigenic peptide fragments of polymorphic for use as immunogens. The antigenic peptide of a polymorphic protein of the invention comprises at least 8 amino acid residues of the amino acid sequence encompassing the polymorphic amino acid and encompasses an epitope of the polymorphic protein such that an antibody raised against the peptide forms a specific immune complex with the polymorphic protein. Preferably, the antigenic peptide comprises at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of polymorphic that are located on the surface of the protein, *e.g.*, hydrophilic regions.

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by injection with the polymorphic protein. An appropriate immunogenic preparation can contain, for example, recombinantly expressed polymorphic protein or a chemically synthesized polymorphic polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against polymorphic proteins can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as protein A chromatography, to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that originates from the clone of a singly hybridoma cell, and that contains only one type of antigen binding site capable of immunoreacting with a particular epitope of a polymorphic protein. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polymorphic protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular polymorphic protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a polymorphic protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methodologies can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*, 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a polymorphic protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotype to a polymorphic protein may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab)²} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab)²} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Additionally, recombinant anti-polymorphic protein antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by

recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988) *J Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060.

In one embodiment, methodologies for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art.

Anti-polymorphic protein antibodies may be used in methods known within the art relating to the detection, quantitation and/or cellular or tissue localization of a polymorphic protein (*e.g.*, for use in measuring levels of the polymorphic protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for polymorphic proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody-derived CDR, are utilized as pharmacologically-active compounds in therapeutic applications intended to treat a pathology in a subject that arises from the presence of the cSNP allele in the subject.

An anti-polymorphic protein antibody (*e.g.*, monoclonal antibody) can be used to isolate polymorphic proteins by a variety of immunochemical techniques, such as immunoaffinity chromatography or immunoprecipitation. An anti-polymorphic protein antibody can facilitate the purification of natural polymorphic protein from cells and of recombinantly produced polymorphic proteins expressed in host cells. Moreover, an anti-polymorphic protein antibody can be used to detect polymorphic protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the polymorphic protein. Anti-polymorphic antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable

substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that unique compositions and methods of use thereof in SNPs in known genes have been described. Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims which follow. In particular, it is contemplated by the inventor that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims.

WHAT IS CLAIMED IS:

1. An isolated polynucleotide selected from the group consisting of:
 - a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7024;
 - b) a fragment of said nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;
 - c) a complementary nucleotide sequence comprising a sequence complementary to one or more of said polymorphic sequences selected from the group consisting of SEQ ID NOS:1-7024; and
 - d) a fragment of said complementary nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.
2. The polynucleotide of claim 1, wherein said polynucleotide sequence is DNA.
3. The polynucleotide of claim 1, wherein said polynucleotide sequence is RNA.
4. The polynucleotide of claim 1, wherein said polynucleotide sequence is between about 10 and about 100 nucleotides in length.
5. The polynucleotide of claim 1, wherein said polynucleotide sequence is between about 10 and about 90 nucleotides in length.
6. The polynucleotide of claim 1, wherein said polynucleotide sequence is between about 10 and about 75 nucleotides in length.
7. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and about 50 bases in length.
8. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and about 40 bases in length.
9. The polynucleotide of claim 1, wherein said polynucleotide is between about 15 and about 30 bases in length.

10. The polynucleotide of claim 1, wherein said polymorphic site includes a nucleotide other than the nucleotide listed in Table 1, column 5 for said polymorphic sequence.
11. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of said polymorphic sequence.
12. The polynucleotide of claim 1, wherein said polymorphic site includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
13. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes the complement of the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
14. An isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is selected from the group consisting of:
 - a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7024 provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence;
 - b) a nucleotide sequence that is a fragment of said polymorphic sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;
 - c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7024, provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and
 - d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

15. The oligonucleotide of claim 14, wherein the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide selected from the group consisting of:
- a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7024, wherein said polymorphic sequence includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence;
 - b) a nucleotide sequence that is a fragment of any of said nucleotide sequences;
 - c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7024, wherein said polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5; and
 - d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.
16. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 10 and about 51 bases in length.
17. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 10 and about 40 bases in length.
18. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 15 and about 30 bases in length.
19. A method of detecting a polymorphic site in a nucleic acid, the method comprising:
- a) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7024, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and
 - b) determining whether said nucleic acid and said oligonucleotide hybridize;

whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphic site in said nucleic acid.

20. The method of claim 19, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.
21. The method of claim 19, wherein said oligonucleotide is between about 10 and about 51 bases in length.
22. The method of claim 19, wherein said oligonucleotide is between about 10 and about 40 bases in length.
23. A method of detecting the presence of a sequence polymorphism in a subject, the method comprising:
 - a) providing a nucleic acid from said subject;
 - b) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7024, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and
 - c) determining whether said nucleic acid and said oligonucleotide hybridize; whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphism in said subject.
24. A method of determining the relatedness of a first and second nucleic acid, the method comprising:
 - a) providing a first nucleic acid and a second nucleic acid;
 - b) contacting said first nucleic acid and said second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7024, or its complement, provided that

the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5;

- c) determining whether said first nucleic acid and said second nucleic acid hybridize to said oligonucleotide; and
 - d) comparing hybridization of said first and second nucleic acids to said oligonucleotide, wherein hybridization of first and second nucleic acids to said nucleic acid indicates the first and second subjects are related.
25. The method of claim 24, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.
26. The method of claim 24, wherein the oligonucleotide is between about 10 and about 51 bases in length.
27. The method of claim 24, wherein the oligonucleotide is between about 10 and about 40 bases in length.
28. The method of claim 24, wherein the oligonucleotide is between about 15 and about 30 bases in length.
29. An isolated polypeptide comprising a polymorphic site at one or more amino acid residues, wherein the protein is encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS:1-7024, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

30. The polypeptide of claim 29, wherein said polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.
31. The polypeptide of claim 29, wherein the polypeptide encoded by said polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.
32. An antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of polymorphic sequences SEQ ID NOS:1-7024, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.
33. The antibody of claim 32, wherein said antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
34. The antibody of claim 32, wherein said antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.
35. A method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject, the method comprising
- a) providing a protein sample from said subject;
 - b) contacting said sample with the antibody of claim 34 under conditions that allow for the formation of antibody-antigen complexes; and
 - c) detecting said antibody-antigen complexes,
- whereby the presence of said complexes indicates the presence of said polypeptide.

36. A method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:
- a) providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or its complement; and
 - b) administering to the subject an effective therapeutic dose of a second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele,
- thereby treating said subject.
37. The method of claim 36, wherein the second nucleic acid sequence comprises a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.
38. A method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:
- a) providing a subject suffering from a pathology associated with aberrant expression of a polymorphic sequence selected from the group consisting of polymorphic sequences SEQ ID NOS:1 - 7024, or its complement; and
 - b) administering to the subject an effective therapeutic dose of a polypeptide,
- wherein said polypeptide is encoded by a polynucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7024, provided that said polymorphic sequence includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.

39. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:
- a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or its complement; and
 - b) administering to the subject an effective dose of the antibody of claim 34, thereby treating said subject.
40. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:
- a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or its complement; and
 - b) administering to the subject an effective dose of an oligonucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7024, provided that said polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for said polymorphic sequence, thereby treating said subject.
41. An oligonucleotide array, comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is chosen from the group consisting of:
- a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7024;
 - b) a nucleotide sequence that is a fragment of any of said nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;

- c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7024; and
 - d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.
42. The array of claim 41, wherein said array comprises about 10 oligonucleotides.
43. The array of claim 41, wherein said array comprises about 100 oligonucleotides.
44. The array of claim 41, wherein said array comprises about 1000 oligonucleotides.

SEQUENCE LISTING

<110> Shimkets, Richard A.
Leach, Martin D.

<120> NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND METHODS OF
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<223> 2 of 2 allelic variants (25 is other entry)

<221> misc_feature
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<223> Accession number cg43299481

<400> 26
caccttcaca gccacccctt tcgcatctc ctccatgtc gggatcttct t 51

<210> 27
<211> 51
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<213> Homo sapiens

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<223> 1 of 2 allelic variants (28 is other entry)

<221> misc_feature
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<223> Accession number cg43941958

<400> 27
ggaaatgcc cattccatag cgcagcttgc actgcacact gctatgaatt c 51

<210> 28
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (27 is other entry)

<221> misc_feature
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<223> Accession number cg43941958

<400> 28
ggaaatgcc cattccatag cgcagcttgc actgcacact gctatgaatt c 51

<210> 29
<211> 51
<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (30 is other entry)

<221> misc_feature

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<223> Accession number cg27363108

<400> 29

gtgcaatgca gttcacacat acctggaatt tatgcagatg ttcagatata g

51

<210> 30

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (29 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27363108

<400> 30

gtgcaatgca gttcacacat acctgaaatt tatgcagatg ttcagatata g

51

<210> 31

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (32 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44921820

<400> 31

tgggtaaagg ggattctggg agttgagagc tctgccaggg tgagatgttt c

51

<210> 32

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (31 is other entry)

<221> misc_feature
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<223> Accession number cg44921820

<400> 32
tgggtaaagg ggattctggg agttgggagc tctgccaggg tgagatgttt c 51

<210> 33
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<212> DNA
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<223> 1 of 2 allelic variants (34 is other entry)

<221> misc_feature
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<223> Accession number cg43988115

<400> 33
atgcttagat gtggtgctgt ggtgctgtgc atttatctaa aatattttta a 51

<210> 34
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (33 is other entry)

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<222> (0)...(0)
<223> Accession number cg43988115

<400> 34
atgcttagat gtggtgctgt ggtgcagtgc atttatctaa aatattttta a 51

<210> 35
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (36 is other entry)

<221> misc_feature
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<223> Accession number cg27783345

<400> 35

tcatgagaca tgcacagccc gcatcccatg ctccgggcgg ggatcgggag c

51

<210> 36

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (35 is other entry)

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<223> Accession number cg27783345

<400> 36

tcatgagaca tgcacagccc gcatcacatg ctccgggcgg ggatcgggag c

51

<210> 37

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (38 is other entry)

<221> misc_feature

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<223> Accession number cg27783345

<400> 37

ccatgctccg ggcggggatc gggagcgtcc gtcaccgac gtggggcgcc g

51

<210> 38

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (37 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27783345

<400> 38

,ccatgctccg ggcggggatc gggaggtccg ctcaccgacg tggggcgccg

50

<210> 39
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<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (40 is other entry)

<221> misc_feature
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<223> Accession number cg43256113

<400> 39
cctcagcttc ctgagtagct gggactacag gtatatacca ctgcacccag c 51

<210> 40
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (39 is other entry)

<221> misc_feature
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<223> Accession number cg43256113

<400> 40
cctcagcttc ctgagtagct gggaccacag gtatatacca ctgcacccag c 51

<210> 41
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (42 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43256113

<400> 41
cttctgagtg agctgggact acaggtatat accactgcac ccagctgtaa g 51

<210> 42
<211> 51
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<213> Homo sapiens

<220>

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<222> (26)...(0)
<223> 2 of 2 allelic variants (41 is other entry)

<221> misc_feature
<222> (0)...(0)
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<400> 42
cttcctgagt agctgggact acaggcatat accactgcac ccagctgtaa g 51

<210> 43
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (44 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44023415

<400> 43
ggaccggaga tggcgccgcc agcggcgcg ggcggcgcg cggcctcgga c 51

<210> 44
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (43 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44023415

<400> 44
ggaccggaga tggcgccgcc agcggggcg ggcggcgcg cggcctcgga c 51

<210> 45
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (46 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg44023415

<400> 45

accggagatg gcgccgccag cggcgcgggc gccggcggcg gcctcggact t

51

<210> 46

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (45 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44023415

<400> 46

accggagatg gcgccgccag cggcgggggc gccggcggcg gcctcggact t

51

<210> 47

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (48 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44929662

<400> 47

agcactttgg gaggccgagg caggcggatc accggaggtc aggagatcga g

51

<210> 48

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (47 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44929662

<400> 48

agcactttgg gaggccgagg caggcagatc accggaggtc aggagatcga g

51

<210> 49

<211> 51
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<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (50 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44929662

<400> 49
gcggatcacc ggaggtcagg agatcgagac catcctggcc aacatggtga a

51

<210> 50
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (49 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44929662

<400> 50
gcggatcacc ggaggtcagg agatcaagac catcctggcc aacatggtga a

51

<210> 51
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (52 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29691725

<400> 51
gggcatgggc cggccctctg tggcgctccg gaacttttcg caatcggcc c

51

<210> 52
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (51 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29691725

<400> 52
gggcatgggc cggcctctg tggcggccg gaacttttcg caatcgccc c 51

<210> 53
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (54 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29691725

<400> 53
aggcgccat caccgcgcg aaaacgttca tccccctcat cgacgggct c 51

<210> 54
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (53 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29691725

<400> 54
aggcgccat caccgcgcg aaaaccttca tccccctcat cgacgggct c 51

<210> 55
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (56 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43985676

<400> 55
aataaaaagta tcataaaaaa acctatTTTT tttccactg tccttccact a 51

<210> 56
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (55 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43985676

<400> 56
aataaaaagta tcataaaaaa acctatTTTT tttccactgt ccttccacta 50

<210> 57
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (58 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44010970

<400> 57
tcctggtccc gaagatgggg ggggggggca gaggagatc ttcacagttt c 51

<210> 58
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (57 is other entry)

<221> misc_feature
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<221> misc_feature.

<222> (0)...(0)
<223> Accession number cg44010970

<400> 58
tcctggtccc gaagatgggg gggggggcag agtgagatct tcacagtttc 50

<210> 59
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (60 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44010970

<400> 59
cctggtcccg aagatggggg gggggggcag agtgagatct tcacagtttc c 51

<210> 60
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (59 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44010970

<400> 60
cctggtcccg aagatggggg gggggggcaga gtgagatctt cacagtttcc 50

<210> 61
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (62 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44010970

<400> 61
ctgggtcccga agatggggggg ggggggcaga gtgagatctt cacagtttcc a 51

<210> 62
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (61 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44010970

<400> 62
ctgggtcccga agatggggggg gggggcagag tgagatcttc acagtttcca 50

<210> 63
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (64 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42718385

<400> 63
tattttgtag agatgggggtt ttgccgtgtt atccaggctg gttttgaact c 51

<210> 64
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (63 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42718385

<400> 64

tattttgtag agatgggggtt ttgccttggt atccaggctg gttttgaact c

51

<210> 65
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (66 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43263821

<400> 65
aaacagcact cctcttctaa aaagatacac aggcgcctt tctcggcagt g

51

<210> 66
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (65 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43263821

<400> 66
aaacagcact cctcttctaa aaagacacac aggcgcctt tctcggcagt g

51

<210> 67
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (68 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg41644093

<400> 67
aagaccagcc tgggcaacat ggggaaaccc catctctaca aaaatacaaa a

51

<210> 68
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (67 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg41644093

<400> 68
aagaccagcc tgggcaacat ggggagaccc catctctaca aaaatacaaa a 51

<210> 69
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (70 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43284479

<400> 69
cagtcgcatt taaaaaaatc aacaacaatg atgataatga aaaaatctga a 51

<210> 70
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (69 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43284479

<400> 70
cagtcgcatt taaaaaaatc aacaagaatg atgataatga aaaaatctga a 51

<210> 71
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (72 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43284479

<400> 71
ggaatgaaga gagaaagcag ctccccaact tcaaaaccat tttggtacct g 51

<210> 72
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (71 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43284479

<400> 72
ggaatgaaga gagaaagcag ctccctaact tcaaaaccat tttggtacct g 51

<210> 73
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (74 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43971784

<400> 73
gcacagctag gtaaaggggg aaaaaatcag atctcaagac agactctttg a 51

<210> 74
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (73 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg43971784

<400> 74

gcacagctag gtaaagggg aaaaatcaga tctcaagaca gactctttga

50

<210> 75

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (76 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43971784

<400> 75

accggcacca aggcattgtct gccctaccca agaagggaga caggccctgg g

51

<210> 76

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (75 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43971784

<400> 76

accggcacca aggcattgtct gccctgcccc agaagggaga caggccctgg g

51

<210> 77

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (78 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42719787

<400> 77

tcaggctccc tagaattacc ccaaaggtca acactatctc agtgccagcc c

51

<210> 78

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (77 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42719787

<400> 78
tcaggctccc tagaattacc ccaaagtca acactatctc agtgccagcc c 51

<210> 79
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (80 is other entry)

<221> misc_feature
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<223> Accession number cg44938005

<400> 79
gcccagaggg aggccatctc agtctgtcca ctgtgggttc agctggtgca t 51

<210> 80
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (79 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44938005

<400> 80
gcccagaggg aggccatctc agtctctcca ctgtgggttc agctggtgca t 51

<210> 81
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 1 of 2 allelic variants (82 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43983675

<400> 81
agcctcatta ttaaaactga aggcattttt tttttctgct gcctttccca a 51

<210> 82
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (81 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43983675

<400> 82
agcctcatta ttaaaactga aggcattttt ttttctgctg cctttcccaa 50

<210> 83
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (84 is other entry)

<221> misc_feature
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<223> Accession number cg43983675

<400> 83
attaaaactg aaggcatttt tttttctgctg tgcctttccc aaagtggta g 51

<210> 84
<211> 50
<212> DNA
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<223> Accession number cg43983675

<400> 84
attaaaactg aaggcatttt tttttctgct gcctttccca aagtggtag 50

<210> 85
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (86 is other entry)

<221> misc_feature
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<223> Accession number cg43983675

<400> 85
tttatttgtg ctttttaagc cattttccca aatgggacta gcatgcttgt t 51

<210> 86
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (85 is other entry)

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<400> 86
tttatttgtg ctttttaagc cattttccca aatgggacta gcatgcttgt t 51

<210> 87
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<222> (0)...(0)
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ccaggaata ctgagagcac taactatgca ctaacctaga ttttcatttc g 51

<210> 88
<211> 51
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ccaggaata ctgagagcac taactgtgca ctaacctaga ttttcatttc g 51

<210> 89
<211> 51
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<223> 1 of 2 allelic variants (90 is other entry)

<221> misc_feature
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<223> Accession number cg44021993

<400> 89
ccatgaagct aatggatgca gcagaactgg taaaacagcc tccggatgtc a 51

<210> 90
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (89 is other entry)

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<400> 90
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<210> 91
<211> 51
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<221> misc_feature
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<400> 91
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<210> 92
<211> 51
<212> DNA
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<400> 92
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<210> 93
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<223> 1 of 2 allelic variants (94 is other entry)

<221> misc_feature
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<223> Accession number cg44012362

<400> 93
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<210> 94
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<400> 94
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<210> 95
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<223> 1 of 2 allelic variants (96 is other entry)

<221> misc_feature
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<223> Accession number cg44012362

<400> 95
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<210> 96
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<212> DNA
<213> Homo sapiens

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<400> 96
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<210> 97
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<223> 1 of 2 allelic variants (98 is other entry)

<221> misc_feature
<222> (0)...(0)
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<400> 97
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<210> 98
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (97 is other entry)

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<222> (0)...(0)
<223> Accession number cg43309765

<400> 98
cctcagactt tcacagatgc gggcgcacgc ccagctgggt cacctgctgc 50

<210> 99
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (100 is other entry)

<221> misc_feature
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<400> 99
ctttcacaga tgcgggcggc atcgccagct gggtcacctg ctgctcagcc c 51

<210> 100
<211> 50
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<400> 100
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<210> 101
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (102 is other entry)

<221> misc_feature
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<400> 101
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<210> 102
<211> 50
<212> DNA
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<223> Accession number cg43294390

<400> 102
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<210> 103
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (104 is other entry)

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<400> 103
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<210> 104
<211> 50
<212> DNA
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<400> 104
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<210> 105
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (106 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44011255

<400> 105
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<210> 106
<211> 51
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<223> 2 of 2 allelic variants (105 is other entry)

<221> misc_feature
<222> (0)...(0)
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<400> 106
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<210> 107
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (108 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926454

<400> 107
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<210> 108
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (107 is other entry)

<221> misc_feature
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<223> Accession number cg43926454

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<210> 109
<211> 51
<212> DNA
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<221> misc_feature
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<223> Accession number cg43993127

<400> 109

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51

<210> 110

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (109 is other entry)

<221> misc_feature

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<223> Accession number cg43993127

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51

<210> 111

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<212> DNA

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<223> 1 of 2 allelic variants (112 is other entry)

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<223> Accession number cg43993127

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51

<210> 112

<211> 51

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<223> 2 of 2 allelic variants (111 is other entry)

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51

<210> 113

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<210> 114
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (113 is other entry)

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<400> 114
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<210> 115
<211> 51
<212> DNA
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<221> misc_feature
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<223> Accession number cg44911042

<400> 115
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<210> 116
<211> 51
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<213> Homo sapiens

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<223> 2 of 2 allelic variants (115 is other entry)

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<223> Accession number cg44911042

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tccccttagg tccctccac aacacatggg aattatggga gtacaattca a

51

<210> 117

<211> 51

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<223> 1 of 2 allelic variants (118 is other entry)

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<222> (0)...(0)

<223> Accession number cg39722830

<400> 117

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51

<210> 118

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (117 is other entry)

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50

<210> 119

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature
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<223> Accession number cg39570416

<400> 119
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<210> 120
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<220>
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<223> 2 of 2 allelic variants (119 is other entry)

<221> misc_feature
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<210> 121
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<220>
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<222> (0)...(0)
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<210> 122
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<222> (26)...(0)
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<223> Accession number cg43281110

<400> 122
cgttgtgacc ttgtctcaaa aaaaaactaa aaaataaagc agttgcatct t 51

<210> 123
<211> 50
<212> DNA
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<221> misc_feature
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<400> 123
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<210> 124
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<221> misc_feature
<222> (0)...(0)
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<400> 124
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<210> 125
<211> 51
<212> DNA
<213> Homo sapiens

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<400> 125
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<210> 126
<211> 51
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<223> 2 of 2 allelic variants (125 is other entry)

<221> misc_feature
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<400> 126
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<210> 127
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<221> misc_feature
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<210> 128
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51

<210> 129

<211> 51

<212> DNA

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<223> Accession number cg43142151

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51

<210> 130

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<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (129 is other entry)

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<222> (0)...(0)

<223> Accession number cg43142151

<400> 130

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51

<210> 131

<211> 51

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<213> Homo sapiens

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<223> 1 of 2 allelic variants (132 is other entry)

<221> misc_feature

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<223> Accession number cg42538578

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51

<210> 132

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<213> Homo sapiens

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<400> 132
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<210> 133
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<400> 133
gcaagactcc acctcaaaaa aaaaaaccac aaaaaaacac aaaaggattc t 51

<210> 134
<211> 50
<212> DNA
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<220>
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<223> Accession number cg42481111

<400> 134
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<210> 135
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<213> Homo sapiens

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<221> misc_feature
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<210> 136
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caaaactcgac tcagcgggtga gctctggcac agttccatga gttgcgaccc t 51

<210> 137
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<221> misc_feature
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<223> Accession number cg38821538

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<210> 138
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (137 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38821538

<400> 138

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51

<210> 139

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> 1 of 2 allelic variants (140 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38821538

<400> 139

aaaaaataat aataataata ataatttttt taaaaagagg tgtttttgag

50

<210> 140

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (139 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38821538

<400> 140

aaaaaataat aataataata ataatatattt ttaaaaagag gtgtttttga g

51

<210> 141

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (142 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38821538

<400> 141
taataataat aataataatt tttttaaaaa gaggtgtttt tgaggtctta 50

<210> 142
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (141 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38821538

<400> 142
taataataat aataataatt tttttaaaaa agaggtgttt ttgaggtctt a 51

<210> 143
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (144 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40038435

<400> 143
tgatcctgca gaggagccaa aaaaaatctt aggtatagaa ctaatacaat t 51

<210> 144
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (143 is other entry)

<221> misc_feature
<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg40038435

<400> 144

tgatcctgca gaggagccaa aaaaatctta ggtatagaac taatacaatt

50

<210> 145

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (146 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43963046

<400> 145

ggccctgtgg ttagcatccc ccacaccat atcagccact agcatttttaa a

51

<210> 146

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (145 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43963046

<400> 146

ggccctgtgg ttagcatccc ccacaccata tcagccacta gcatttttaa

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<210> 147

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (148 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43963046

<400> 147
ccctgtgggtt agcatccccc acacccatat cagccactag catttttaaag a 51

<210> 148
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (147 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43963046

<400> 148
ccctgtgggtt agcatccccc acaccatata agccactagc attttaaaga 50

<210> 149
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (150 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43979733

<400> 149
aaaatgtatg atcaagtccc agaaaacttt gccttcccaa ggaatgtgtt t 51

<210> 150
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (149 is other entry)

<221> misc_feature
<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43979733

<400> 150

aaaatgtatg atcaagtccc agaaactttg ccttcccaag gaatgtgtt

50

<210> 151

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (152 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43979733

<400> 151

ccaaaaaatca cattctctct ctctctctc tcctctctac cattctctc a

51

<210> 152

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (151 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43979733

<400> 152

ccaaaaaatca cattctctct ctctccctct cctctctacc attctctca

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<210> 153

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (154 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43979733

<400> 153
cagtaagaaa accaggagac tccttctgaa aggcttccac ctgggaggaa a 51

<210> 154
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (153 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43979733

<400> 154
cagtaagaaa accaggagac tccttatgaa aggcttccac ctgggaggaa a 51

<210> 155
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (156 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42286566

<400> 155
ctgggattac aggcattgagc caccgtgcct ggccagaaaa ttgtaaacac a 51

<210> 156
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (155 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42286566

<400> 156
ctgggattac aggcattgagc caccgggcct ggccagaaaa ttgtaaacac a 51

<210> 157
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (158 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42286566

<400> 157
gattacaggc atgagccacc gtgcctggcc agaaaattgt aaacacacac a 51

<210> 158
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (157 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42286566

<400> 158
gattacaggc atgagccacc gtgcccggcc agaaaattgt aaacacacac a 51

<210> 159
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (160 is other entry)

<221> misc_feature
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<223> Accession number cg42286566

<400> 159
tgcctggcca gaaaattgta aacacacaca aactctcaag tggcctaatt c 51

<210> 160
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (159 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42286566

<400> 160
tgcctggcca gaaaattgta aacacgcaca aactctcaag tggcctaatt c 51

<210> 161
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (162 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42286566

<400> 161
ctctcaccaa accaatcaca atacagataa aagagaataa cttgtgttca t 51

<210> 162
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (161 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42286566

<400> 162
ctctcaccaa accaatcaca atacaaataa aagagaataa cttgtgttca t 51

<210> 163
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (164 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg42286566

<400> 163
caatacagat aaaagagaat aacttggtgtt catttttgta caaacaaaaa a 51

<210> 164
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (163 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42286566

<400> 164
caatacagat aaaagagaat aacttatgtt catttttgta caaacaaaaa a 51

<210> 165
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (166 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42286566

<400> 165
atacagataa aagagaataa cttgtgttca tttttgtaca aacaaaaaag a 51

<210> 166
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (165 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42286566

<400> 166
atacagataa aagagaataa cttgtattca tttttgtaca aacaaaaaag a 51

<210> 167
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (168 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42286566

<400> 167
cagataaaag agaataactt gtgttcattt ttgtacaaac aaaaaagata t 51

<210> 168
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (167 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42286566

<400> 168
cagataaaag agaataactt gtgttaattt ttgtacaaac aaaaaagata t 51

<210> 169
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (170 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42286566

<400> 169
ttcatttttg tacaacaaa aaagatataa attgtgaatg atgcatgatt 50

<210> 170
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (169 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42286566

<400> 170
ttcatttttg tacaacaaa aaagactata aattgtgaat gatgcatgat t 51

<210> 171
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (172 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42468290

<400> 171
caaaccaaac aaccacaaca aaaaaatccc tcacttttgt ttctgttta t 51

<210> 172
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (171 is other entry).

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42468290

<400> 172
caaaccaaac aaccacaaca aaaaatccct cacttttgtt ttctgtttat 50

<210> 173
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (174 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44010179

<400> 173
tcccataggt agcagtcgct gtgggcaggt ggaaggtgcc cgtccctcta g 51

<210> 174
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (173 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44010179

<400> 174
tcccataggt agcagtcgct gtgggaggtg gaaggtgccc gtcctctag 50

<210> 175
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (176 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42927851

<400> 175
cctaggagga agacaagctt gaaggacgac ccttaataaa gagcttctag g 51

<210> 176
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (175 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42927851

<400> 176
cctaggagga agacaagctt gaagggcgac ccttaataaa gagcttctag g 51

<210> 177
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (178 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43998776

<400> 177
tgatggggag ttttagagga gcaataaaaa acttccttct ttgtgcttgt g 51

<210> 178
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (177 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43998776

<400> 178
tgatggggag ttttagagga gcaatcaaaa acttccttct ttgtgcttgt g 51

<210> 179
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (180 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg43923142

<400> 179
cccactcgcg ttctgagccc cgagagcgtc ccgcacgctc agtttggtg a 51

<210> 180
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (179 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43923142

<400> 180
cccactcgcg ttctgagccc cgagaccgtc ccgcacgctc agtttggtg a 51

<210> 181
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (182 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg10053419

<400> 181
gggggaggta ggcagtaccc cccctgctc ctgtggggaa ataggggctt a 51

<210> 182
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (181 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg10053419

<400> 182
gggggaggta ggcagtaccc ccccgctcc tgtggggaaa taggggctta 50

<210> 183
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (184 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg10333107

<400> 183
tgccctgag gtcaagcaga cccacaccgt cgaccgggtt gtcgtcgtaa c 51

<210> 184
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (183 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg10333107

<400> 184
tgccctgag gtcaagcaga cccaccccggt cgaccgggtt gtcgtcgtaa c 51

<210> 185
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (186 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg10353763

<400> 185
tggcaggctt tgtcagtgtt tcagcgggta agaaatcttg actagtagga a 51

<210> 186
<211> 51
<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (185 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg10353763

<400> 186
tggcaggctt tgtcagtgtt tcagcaggta agaaatcttg actagtagga a 51

<210> 187
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (188 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg10854402

<400> 187
ttgtgatctc aacaacaaca ttgaaaacag caggagcacc aggaccgatc t 51

<210> 188
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (187 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg10854402

<400> 188
ttgtgatctc aacaacaaca ttgaatacag caggagcacc aggaccgatc t 51

<210> 189
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (190 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg11763542

<400> 189
aggctgaggc aggagaatcg cttgagcctg ggaggcagag gttgcagtga g 51

<210> 190
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (189 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg11763542

<400> 190
aggctgaggc aggagaatcg cttgaacctg ggaggcagag gttgcagtga g 51

<210> 191
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (192 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg11763542

<400> 191
cgcttgagcc tgggaggcag aggttgagc gagccaagat catgccactg c 51

<210> 192
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (191 is other entry)

<221> misc_feature
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<223> Accession number cg11763542

<400> 192

cgcttgagcc tgggaggcag aggttttcagt gagccaagat catgccactg c 51

<210> 193
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (194 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg11794373

<400> 193
ccggaatacc ttatactttt tccccctttt ttttggggga aggaatgtgt g 51

<210> 194
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (193 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg11794373

<400> 194
ccggaatacc ttatactttt tccccctttt ttttggggga aggaatgtgt g 51

<210> 195
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (196 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg11801777

<400> 195
accctatcaa cccattaaaa tggatttttaa tgaattgata ataggggctc a 51

<210> 196
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (195 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg11801777

<400> 196
accctatcaa cccattaaaa tggatattaa tgaattgata ataggggctc a 51

<210> 197
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (198 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg11801777

<400> 197
tcaatcagct gataaacccc ctaaaaaagt tgcggaaacc caattgttac a 51

<210> 198
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (197 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg11801777

<400> 198
tcaatcagct gataaacccc ctaaagaagt tgcggaaacc caattgttac a 51

<210> 199
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (200 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg12991942

<400> 199
agagttttat tcctttgagg gccacagaag aaagtagtct agctctcttc a 51

<210> 200
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (199 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg12991942

<400> 200
agagttttat tcctttgagg gccactgaag aaagtagtct agctctcttc a 51

<210> 201
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (202 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg13084930

<400> 201
ttgttggtgcg tgtggtcaag atgctgactc acgatcacag tgggctcttc g 51

<210> 202
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (201 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg13084930

<400> 202
ttgttggtgcg tgtggtcaag atgctaactc acgatcacag tgggctcttc g 51

<210> 203
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (204 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg13086160

<400> 203
actaagcaca ggctcagccc cggtcgccat gcgcccaggc tcggttatca g

51

<210> 204
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (203 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg13086160

<400> 204
actaagcaca ggctcagccc cggtcaccat gcgcccaggc tcggttatca g

51

<210> 205
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (206 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg13502101

<400> 205
gcgggggttaa cgggtcagga gacaagaagg tgggtggtagt tgggtcgtag a

51

<210> 206
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (205 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg13502101

<400> 206
gcgggggtaa cgggtcagga gacaaaaagg tgggtgtagt tgggtcgtag a 51

<210> 207
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (208 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg14203037

<400> 207
agtaacagaa atataacaaa attggcataa acatttgggt atctgttaac c 51

<210> 208
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (207 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg14203037

<400> 208
agtaacagaa atataacaaa attggaataa acatttgggt atctgttaac c 51

<210> 209
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (210 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg14203037

<400> 209
agaaatataa caaaattggc ataaacattt gggtatctgt taaccaagag t 51

<210> 210
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (209 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg14203037

<400> 210
agaaatataa caaaattggc ataaaaattt gggtatctgt taaccaagag t 51

<210> 211
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (212 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg14203037

<400> 211
cataaacatt tgggtatctg ttaaccaaga gtgtgaagat aaggtagttc c 51

<210> 212
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (211 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg14203037

<400> 212
cataaacatt tgggtatctg ttaacaaaga gtgtgaagat aaggtagttc c 51

<210> 213
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (214 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg14369904

<400> 213
gcggaacctc gcgcttcgcc cgggggacaa tccgaagtcg gcgctatgga a 51

<210> 214
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (213 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg14369904

<400> 214
gcggaacctc gcgcttcgcc cgggggacaat ccgaagtcg cgctatggaa 50

<210> 215
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (216 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg14395282

<400> 215
caccctgat gccggcctgg ctgggaatgg gcccgctctg cacctcgagc t 51

<210> 216
<211> 51

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (215 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg14395282

<400> 216
cacccctgat gccggcctgg ctgggggatgg gcccgctcctg cacctcgagc t 51

<210> 217
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (218 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg14395282

<400> 217
cacctcgagc tagggcaaga agaggcagag ctggaggagt tcctgtgccc 50

<210> 218
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (217 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg14395282

<400> 218
cacctcgagc tagggcaaga agaggacaga gctggaggag ttctgtgcc c 51

<210> 219
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (220 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg14396111

<400> 219
tcagatatgg aactacatga gatctgtagc gaactgcgga ggatcagaca c 51

<210> 220
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (219 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg14396111

<400> 220
tcagatatgg aactacatga gatcttagcg aactgcggag gatcagacac 50

<210> 221
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (222 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16311688

<400> 221
gttctcgggt gccgtcgtg tgcgcttcgc tgctgtgacg ctcaactgggc g 51

<210> 222
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (221 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16311688

<400> 222
gttctcgggt gccgtcgtg tgcgcctcgc tgctgtgacg ctcaactgggc g 51

<210> 223
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (224 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16311688

<400> 223
gcgtccagtc ccacagttcg accacatccg gcggctccgt gcccgcgacc a 51

<210> 224
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (223 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16311688

<400> 224
gcgtccagtc ccacagttcg accacttccg gcggctccgt gcccgcgacc a 51

<210> 225
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (226 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg16311688

<400> 225

tgtccattgc gggtagt ttt cggggcgcgc gaagccgggg gttccactag g

51

<210> 226

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (225 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg16311688

<400> 226

tgtccattgc gggtagt ttt cggggcgcgc gaagccgggg gttccactag g

51

<210> 227

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (228 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg16311688

<400> 227

gggcgcgcga agccgggggt tccactaggg ctgggagccc gacaccgagc g

51

<210> 228

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (227 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg16311688

<400> 228

gggcgcgcga agccgggggt tccacgaggg ctgggagccc gacaccgagc g

51

<210> 229

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (230 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16392609

<400> 229
tgctcattga tccctacgac aagggtgtca tggctcatga caggggtgggc g

51

<210> 230
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (229 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16392609

<400> 230
tgctcattga tccctacgac aagggtgtca tggctcatga caggggtgggc g

51

<210> 231
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (232 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16392609

<400> 231
cctacgacaa ggttggtcatg gctcatgaca ggggtgggcgc ggttcccact g

51

<210> 232
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 2 of 2 allelic variants (231 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16392609

<400> 232
cctacgacaa ggttgatcatg gctcaagaca ggggtggcgc ggttcccact g 51

<210> 233
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (234 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16392609

<400> 233
acaaggttgt catggctcat gacaggggtg tcgcgggtcc cactgagggt g 51

<210> 234
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (233 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16392609

<400> 234
acaaggttgt catggctcat gacagagtgg tcgcgggtcc cactgagggt g 51

<210> 235
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (236 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16697187

<400> 235
atgtgttcacat tgccatcggg tcgatacctgc tcatacactgg attcggttgac g 51

<210> 236
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (235 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16697187

<400> 236
atgtgttcacat tgccatcggg tcgattctgc tcatacactgg attcggttgac g 51

<210> 237
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (238 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16843354

<400> 237
aaaagactag taacggcgaa gccgacgaga cagttatctg ccacgttgct g 51

<210> 238
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (237 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16843354

<400> 238
aaaagactag taacggcgaa gccgatgaga cagttatctg ccacgttgct g 51

<210> 239
<211> 51

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (240 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16845019

<400> 239
cctctctgat atttgggtgg ggaagggggg ttgggggtcc tctttcttca a

51

<210> 240
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (239 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg16845019

<400> 240
cctctctgat atttgggtgg ggaagtgggg ttgggggtcc tctttcttca a

51

<210> 241
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (242 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg17201640

<400> 241
ccagttcata ttgatccaat ttctagaaa caaatgctga agttcattgc a

51

<210> 242
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 2 of 2 allelic variants (241 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg17201640

<400> 242

ccagttcata ttgatccaat ttctaaaaaa caaatgctga agttcattgc a

51

<210> 243

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (244 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg17872027

<400> 243

tgacttcaag tgatcctcct gcctcggcct ctcaaagtgc tgggattaca g

51

<210> 244

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (243 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg17872027

<400> 244

tgacttcaag tgatcctcct gcctcagcct ctcaaagtgc tgggattaca g

51

<210> 245

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (246 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg17872027

<400> 245
caagtgatcc tcttgctcgc gcctctcaaa gtgctgggat tacagatatg a 51

<210> 246
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (245 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg17872027

<400> 246
caagtgatcc tcttgctcgc gcctcccaaa gtgctgggat tacagatatg a 51

<210> 247
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (248 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg17964567

<400> 247
gcctgtcca cactcagctc ccacagcctc accctgtccc accagacaca c 51

<210> 248
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (247 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg17964567

<400> 248
gcctgtcca cactcagctc ccacatcctc accctgtccc accagacaca c 51

<210> 249
<211> 46
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (250 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg17964567

<400> 249

gtcccaccag acacacacag cttagtgcaca cagattctgg aagctt

46

<210> 250

<211> 46

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (249 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg17964567

<400> 250

gtcccaccag acacacacag cttagcgaca cagattctgg aagctt

46

<210> 251

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (252 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg17964567

<400> 251

gctgaggcct gagcccatca aagacgagaa ctgactgagc acacctgggc a

51

<210> 252

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (251 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg17964567

<400> 252
gctgaggcct gagcccatca aagacaagaa ctgactgagc acacctgggc a 51

<210> 253
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (254 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19426737

<400> 253
cgttcagctc tgccaatggg aagccggagg cgcttccttc agcgagaagg t 51

<210> 254
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (253 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19426737

<400> 254
cgttcagctc tgccaatggg aagccagagg cgcttccttc agcgagaagg t 51

<210> 255
<211> 40
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (15)...(0)
<223> 1 of 2 allelic variants (256 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19540358

<400> 255

nggagagacg acaaggggtga agggaaagaa tgactgatgg

40

<210> 256

<211> 40

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (15)...(0)

<223> 2 of 2 allelic variants (255 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg19540358

<400> 256

nggagagacg acaacgggtga agggaaagaa tgactgatgg

40

<210> 257

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (258 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg19636928

<400> 257

ctatcagagg gctccatcac tccatcgtaa ggaggcagct ggtggcgagt c

51

<210> 258

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (257 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg19636928

<400> 258

ctatcagagg gctccatcac tccattgtaa ggaggcagct ggtggcgagt c

51

<210> 259

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (260 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19650073

<400> 259
agctttggca gaggaccctc tgcacgcttc ctctcctcta gccagagctt c 51

<210> 260
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (259 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19650073

<400> 260
agctttggca gaggaccctc tgcacacttc ctctcctcta gccagagctt c 51

<210> 261
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (262 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19847826

<400> 261
acgccgaccg gatcgtcgat cccattactc gggatctgct ggaatccctg g 51

<210> 262
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (261 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19847826

<400> 262
acgccgaccg gatcgtcgat cccatcactc gggatctgct ggaatccctg g 51

<210> 263
<211> 39
<212> DNA
<213> Homo sapiens

<220>
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<222> (14)...(0)
<223> 1 of 2 allelic variants (264 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19847826

<400> 263
acgcgtccgc tccggatttc gttgacgagc tgcgctcag 39

<210> 264
<211> 39
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (14)...(0)
<223> 2 of 2 allelic variants (263 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19847826

<400> 264
acgcgtccgc tcccgatttc gttgacgagc tgcgctcag 39

<210> 265
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (266 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19847826

<400> 265
ctcgggatct gctggaatcc ctggttcgcg aagccggcga ggctgcggtg a 51

<210> 266
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (265 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19847826

<400> 266
ctcgggatct gctggaatcc ctggtccgcg aagccggcga ggctgcggtg a 51

<210> 267
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (268 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19847826

<400> 267
ctgctggaat ccctggttcg cgaagccggc gaggctgcgg tgatcttggg t 51

<210> 268
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (267 is other entry)

<221> misc_feature
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<223> Accession number cg19847826

<400> 268
ctgctggaat ccctggttcg cgaagtcggc gaggctgcgg tgatcttggg t 51

<210> 269
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (270 is other entry)

<221> misc_feature
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<223> Accession number cg19847826

<400> 269
tcacccatct gccccgacga cccagtaaac gtccccggct gttcctcatt g 51

<210> 270
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (269 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19847826

<400> 270
tcacccatct gccccgacga cccagcaaac gtccccggct gttcctcatt g 51

<210> 271
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (272 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19848544

<400> 271
accgcgacgc gattctggcc ttccccgttg agacggtgta taccgccgac c 51

<210> 272
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (271 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg19848544

<400> 272
accgcgacgc gattctggcc ttccctgttg agacggtgta taccgccgac c 51

<210> 273
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (274 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19848544

<400> 273
tctggccttc cccgttgaga cgggtgtatac cgccgaccgc cccgtgcagc g 51

<210> 274
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (273 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19848544

<400> 274
tctggccttc cccgttgaga cgggtgcatac cgccgaccgc cccgtgcagc g 51

<210> 275
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (276 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19848544

<400> 275
taccgccgac cgccccgtgc agcgccctggc cgaaatcggt gccgagtacg a 51

<210> 276
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (275 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19848544

<400> 276
taccgccgac cgccccgtgc agcgcttggc cgaaatcggt gccgagtacg a

51

<210> 277
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (278 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19848544

<400> 277
acgaaccggt tgaagtcac atgggacttc cggtcgccct taacgggact g

51

<210> 278
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (277 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19848544

<400> 278
acgaaccggt tgaagtcac atggggcttc cggtcgccct taacgggact g

51

<210> 279
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (280 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19848544

<400> 279
ttgaagtcacat catgggactt ccggtcgccc ttaacgggac tgagcagttg g 51

<210> 280
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (279 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19848544

<400> 280
ttgaagtcacat catgggactt ccggttgccc ttaacgggac tgagcagttg g 51

<210> 281
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (282 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19848544

<400> 281
cggacacgtg tctgtgcggt gtgaggcttg ccatcgactg gggaaaggca c 51

<210> 282
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (281 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg19848544

<400> 282

cggaacacgtg tctgtgacgtg gtgagacttg ccatcgactg gggaaaggca c

51

<210> 283

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (284 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg19869623

<400> 283

cagagtctgt gagcgccag gaggcacct gctcgactgg cccgtcctct c

51

<210> 284

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (283 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg19869623

<400> 284

cagagtctgt gagcgccag gaggcacctg ctgcactggc cccgtcctctc

50

<210> 285

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (286 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg19891431

<400> 285
cttcaggagg ccaaggaggg aggatagact aaggtgagtt caagaccagc c 51

<210> 286
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (285 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19891431

<400> 286
cttcaggagg ccaaggaggg aggatggact aaggtgagtt caagaccagc c 51

<210> 287
<211> 51
<212> DNA
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<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (288 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19891431

<400> 287
caagaccagc ctgggcaata cagtggagacc ctgcctctat aaaaaaaaaat t 51

<210> 288
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (287 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19891431

<400> 288
caagaccagc ctgggcaata cagtgggacc ctgcctctat aaaaaaaaaat t 51

<210> 289
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (290 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg19906230

<400> 289

cagactgaca agcaagggat tttttccact caccgtcagt gggatgggtc t

51

<210> 290

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (289 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg19906230

<400> 290

cagactgaca agcaagggat tttttccact caccgtcagt gggatgggtc t

51

<210> 291

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (292 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg19906230

<400> 291

acacgattat ttcacaaaaa gaaactttct gtgggacgtg cctgggcgac t

51

<210> 292

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (291 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19906230

<400> 292
acacgattat ttcacaaaaa gaaaccttct gtgggacgtg cctgggcgac t 51

<210> 293
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (294 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19906230

<400> 293
gccagcaaaa ctgagaacct tgttcgcaaa tccgtaccct ctccaaggc a 51

<210> 294
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (293 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19906230

<400> 294
gccagcaaaa ctgagaacct tgttctcaaa tccgtaccct ctccaaggc a 51

<210> 295
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (296 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg19906230

<400> 295

aaactgagaa ccttgttcgc aaatccgtac cctctcccaa ggcagcctca g

51

<210> 296

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (295 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg19906230

<400> 296

aaactgagaa ccttgttcgc aaatctgtac cctctcccaa ggcagcctca g

51

<210> 297

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (298 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20177119

<400> 297

ctcagaacct ggagatcagg ttttgaccgg tgagccagcc cgggaccttc c

51

<210> 298

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (297 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20177119

<400> 298

ctcagaacct ggagatcagg ttttggccgg tgagccagcc cgggaccttc c

51

<210> 299

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (300 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20177119

<400> 299
cagccgacgt cgcggctgac gacgtccccc ccaaaccgt tggcgatac c 51

<210> 300
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (299 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20177119

<400> 300
cagccgacgt cgcggctgac gacgtccccc caaatccgtt gggcgatacc 50

<210> 301
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (302 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20177119

<400> 301
acgtcgcggc tgacgacgtc ccccccaaat ccgttgggcg ataccgcct c 51

<210> 302
<211> 50
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (301 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20177119

<400> 302
acgtcgcggc tgacgacgtc cccccaaatc cgttgggcga taccgcctc

50

<210> 303
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (304 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20177119

<400> 303
tccccccaa atccgttggg cgataccgc ctgaaccaa cccgggattg a

51

<210> 304
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (303 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20177119

<400> 304
tccccccaa atccgttggg cgatatccgc ctgaaccaa cccgggattg a

51

<210> 305
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 1 of 2 allelic variants (306 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20177119

<400> 305
ttgggcgata cccgcctcga accaaccg gattgacccc gggagatcca a 51

<210> 306
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (305 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20177119

<400> 306
ttgggcgata cccgcctcga accaatccg gattgacccc gggagatcca a 51

<210> 307
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (308 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20283978

<400> 307
aggaaacacc agatttgccc aggaagacag tgggatggct ttgatatctc t 51

<210> 308
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (307 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20283978

<400> 308
aggaaacacc agatttgccc aggaatacag tgggatggct ttgatatctc t 51

<210> 309
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (310 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20287156

<400> 309
cggcggccca atctgccgga cgtgacgccg ggatgtcgct gggacttatg t 51

<210> 310
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (309 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20287156

<400> 310
cggcggccca atctgccgga cgtgatgccg ggatgtcgct gggacttatg t 51

<210> 311
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (312 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20287300

<400> 311
ttgcggcccg atttcgactt tatcagtctc ttccacggag tcgacgagag a 51

<210> 312
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (311 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20287300

<400> 312

ttgccggccg atttcgactt tatcaatctc ttccacggag tcgacgagag a

51

<210> 313

<211> 51

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<223> 1 of 2 allelic variants (314 is other entry)

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<223> Accession number cg20289946

<400> 313

tccaggctgt gagcgtgcaa gaacagcacg gcggcgaaag agaaccggt a

51

<210> 314

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (313 is other entry)

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<222> (0)...(0)

<223> Accession number cg20289946

<400> 314

tccaggctgt gagcgtgcaa gaacaccacg gcggcgaaag agaaccggt a

51

<210> 315

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (316 is other entry)

<221> misc_feature
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<400> 315
gagcgtgcaa gaacagcacg gggcgaaaag agaaccgggt acgcggtgcg g 51

<210> 316
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<223> 2 of 2 allelic variants (315 is other entry)

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<223> Accession number cg20289946

<400> 316
gagcgtgcaa gaacagcacg gggccaaaag agaaccgggt acgcggtgcg g 51

<210> 317
<211> 51
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<223> 1 of 2 allelic variants (318 is other entry)

<221> misc_feature
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<223> Accession number cg20375502

<400> 317
ggatctgtgg ccacctctc aagggttgcc acacgcacca ggtcctgact g 51

<210> 318
<211> 51
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<223> 2 of 2 allelic variants (317 is other entry)

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<223> Accession number cg20375502

<400> 318

ggatctgtgg ccacctcctc aaggggtgcc acacgcacca ggtcctgact g

51

<210> 319
<211> 51
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<223> 1 of 2 allelic variants (320 is other entry)

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<400> 319
cgcaccaggt cctgactggg agtccggccc ccagggcctg tggatggctg g

51

<210> 320
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<223> 2 of 2 allelic variants (319 is other entry)

<221> misc_feature
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<400> 320
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51

<210> 321
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<223> 1 of 2 allelic variants (322 is other entry)

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<400> 321
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51

<210> 322
<211> 50
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<221> misc_feature
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<400> 322
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<210> 323
<211> 51
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<223> 1 of 2 allelic variants (324 is other entry)

<221> misc_feature
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<400> 323
gggcccggtg gggctcctgcg gggacgcggg cgaggacggc gcggacgagg c 51

<210> 324
<211> 50
<212> DNA
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<221> misc_feature
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<400> 324
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<210> 325
<211> 51

<212> DNA
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<220>
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<223> 1 of 2 allelic variants (326 is other entry)

<221> misc_feature
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<223> Accession number cg20436638

<400> 325
ctaccaggcc gccgccttcg ccggatcccg tcccgacctt gagttgggtc a

51

<210> 326
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (325 is other entry)

<221> misc_feature
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<400> 326
ctaccaggcc gccgccttcg ccggaaccg tcccgacctt gagttgggtc a

51

<210> 327
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<213> Homo sapiens

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<223> 1 of 2 allelic variants (328 is other entry)

<221> misc_feature
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<400> 327
ccgccgcctt ccgccgatcc cgtcccgacc ttgagttggt tcagctgaat t

51

<210> 328
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<212> DNA
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<223> 2 of 2 allelic variants (327 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20436638

<400> 328

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<210> 329

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (330 is other entry)

<221> misc_feature

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<223> Accession number cg20440553

<400> 329

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51

<210> 330

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (329 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20440553

<400> 330

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51

<210> 331

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<223> 1 of 2 allelic variants (332 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20442259

<400> 331
cggccactcc ccatacgcta tgaggcgacc atcatcacct tcaccgaaca a 51

<210> 332
<211> 50
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<223> 2 of 2 allelic variants (331 is other entry)

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<223> Accession number cg20442259

<400> 332
cggccactcc ccatacgcta tgagggacca tcatcacctt caccgaacaa 50

<210> 333
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<223> 1 of 2 allelic variants (334 is other entry)

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<400> 333
ggggagagag gcgggaggga cactggcctg gagagaggcg ggagggacgc t 51

<210> 334
<211> 51
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<221> misc_feature
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<400> 334
ggggagagag gcgggaggga cactgacctg gagagaggcg ggagggacgc t 51

<210> 335
<211> 51
<212> DNA
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<223> Accession number cg20457127

<400> 335
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<210> 336
<211> 50
<212> DNA
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<400> 336
cgaggaaatg acctccttcg cggtaccgac cagcgatcca ccgacgagac 50

<210> 337
<211> 51
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<222> (26)...(0)
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<223> Accession number cg20549295

<400> 337
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<210> 338

<211> 51
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<223> 2 of 2 allelic variants (337 is other entry)

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<223> Accession number cg20549295

<400> 338
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<210> 339
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<223> 1 of 2 allelic variants (340 is other entry)

<221> misc_feature
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<223> Accession number cg20562029

<400> 339
ttggtctttt gagatggttt tcagactttt gcattatggc aaccaactga c 51

<210> 340
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (339 is other entry)

<221> misc_feature
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<223> Accession number cg20562029

<400> 340
ttggtctttt gagatggttt tcagattttt gcattatggc aaccaactga c 51

<210> 341
<211> 51
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (342 is other entry)

<221> misc_feature
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<223> Accession number cg20562607

<400> 341
tgagcttggt cacaccctct ggcaggaagt tcagaaggga acacagaacc a 51

<210> 342
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<212> DNA
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<223> 2 of 2 allelic variants (341 is other entry)

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<223> Accession number cg20562607

<400> 342
tgagcttggt cacaccctct ggcagaaagt tcagaaggga acacagaacc a 51

<210> 343
<211> 51
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<223> 1 of 2 allelic variants (344 is other entry)

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<223> Accession number cg44921008

<400> 343
aaaccaagt gtggcaaagg aactcattgc tctcgaaatg catatatgtt g 51

<210> 344
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (343 is other entry)

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<223> Accession number cg44921008

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aaaccaagt gtggcaaagg aactcgttgc tctcgaaatg catatatgtt g 51

<210> 345
<211> 51
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<221> misc_feature
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<223> Accession number cg44921017

<400> 345
acatctgttt agccacagaa agcattgggc catactcact gcagaagata a 51

<210> 346
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (345 is other entry)

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<223> Accession number cg44921017

<400> 346
acatctgttt agccacagaa agcatcgggc catactcact gcagaagata a 51

<210> 347
<211> 51
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<223> 1 of 2 allelic variants (348 is other entry)

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<223> Accession number cg44921017

<400> 347
gataagactt cctcagaatc ttattcggtt agtgcaactca attttacttc a 51

<210> 348
<211> 51

<212> DNA
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<223> 2 of 2 allelic variants (347 is other entry)

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<223> Accession number cg44921017

<400> 348
gataagactt cctcagaatc ttatttggtt agtgactca attttacttc a 51

<210> 349
<211> 51
<212> DNA
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<400> 349
ggatgcggac atcgacaagg ccttgcagga tctgctgggg caccttgaag c 51

<210> 350
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (349 is other entry)

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<400> 350
ggatgcggac atcgacaagg ccttgaagga tctgctgggg caccttgaag c 51

<210> 351
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (352 is other entry)

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<223> Accession number cg44921180

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tctgctgggg caccttgaag cggacatagg agcagagctg aagcatttca c

51

<210> 352

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (351 is other entry)

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tctgctgggg caccttgaag cggacgtagg agcagagctg aagcatttca c

51

<210> 353

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (354 is other entry)

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<400> 353

tgaagcggac ataggagcag agctgaagca ttctactcat ctcttctggg g

51

<210> 354

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (353 is other entry)

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<223> Accession number cg44921180

<400> 354
tgaagcggac ataggagcag agctgcagca tttcactcat ctcttctggg g 51

<210> 355
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<400> 355
ggacatagga gcagagctga agcatttcac tcatctcttc tggggtagac g 51

<210> 356
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<212> DNA
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<223> 2 of 2 allelic variants (355 is other entry)

<221> misc_feature
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<400> 356
ggacatagga gcagagctga agcatctcac tcatctcttc tggggtagac g 51

<210> 357
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (358 is other entry)

<221> misc_feature
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<400> 357
gctgaagcat ttcactcatc tcttctgggg tagacgggat caaggaatc t 51

<210> 358
<211> 51
<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (357 is other entry)

<221> misc_feature

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<223> Accession number cg44921180

<400> 358
gctgaagcat ttactcatc tcttcgggg tagacgggat caagggaatc t 51

<210> 359

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (360 is other entry)

<221> misc_feature

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<223> Accession number cg44921180

<400> 359
gcatttcact catctcttct ggggtagacg ggatcaaggg aatcttctcc a 51

<210> 360

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (359 is other entry)

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<222> (0)...(0)

<223> Accession number cg44921180

<400> 360
gcatttcact catctcttct ggggtggacg ggatcaaggg aatcttctcc a 51

<210> 361

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<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (362 is other entry)

<221> misc_feature
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<400> 361
tctcttctgg ggtagacggg atcaagggaa tcttctccac ggcggcagag c 51

<210> 362
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<223> 2 of 2 allelic variants (361 is other entry)

<221> misc_feature
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<400> 362
tctcttctgg ggtagacggg atcaaaggaa tcttctccac ggcggcagag c 51

<210> 363
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (364 is other entry)

<221> misc_feature
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<223> Accession number cg44921180

<400> 363
tcctccctgg tcttgcagcc aatgggctgc agtcatacat gggctctctat g 51

<210> 364
<211> 51
<212> DNA
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<220>
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<221> misc_feature
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<400> 364

tcctccctgg tcttgcagcc aatggactgc agtcatacat gggctcttat g

51

<210> 365

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (366 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44921801

<400> 365

gcctgggcaa caagagtga actccatctc aaaaaaaaaa aaaaaaaaag a

51

<210> 366

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (365 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44921801

<400> 366

gcctgggcaa caagagtga actccgtctc aaaaaaaaaa aaaaaaaaag a

51

<210> 367

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<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (368 is other entry)

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<223> Accession number cg44921847

<400> 367

aataatatgt taacataaac ataacaacac acatattatt tttctacccc t

51

<210> 368

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature
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<223> Accession number cg44921847

<400> 368
aataatatgt taacataaac ataacgacac acatattatt tttctacccc t 51

<210> 369
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (370 is other entry)

<221> misc_feature
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<223> Accession number cg44921882

<400> 369
aaaacttgaa ctcttctaga cagataccga gtggcaatct gggtatgttt g 51

<210> 370
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (369 is other entry)

<221> misc_feature
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<223> Accession number cg44921882

<400> 370
aaaacttgaa ctcttctaga cagatcccga gtggcaatct gggtatgttt g 51

<210> 371
<211> 51
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<213> Homo sapiens

<220>
<221> misc_feature
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<223> 1 of 2 allelic variants (372 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44921882

<400> 371
acagataccg agtggcaatc tgggtatgtt tggcaatagc ggagcagcac a 51

<210> 372
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (371 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44921882

<400> 372
acagataccg agtggcaatc tgggtgtgtt tggcaatagc ggagcagcac a 51

<210> 373
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (374 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44921986

<400> 373
cctgaatggg gtggtagatt ttttttctta aaaaaatttt tttgtttttt t 51

<210> 374
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (373 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg44921986

<400> 374

cctgaatggg gtggtagatt tttttcttaa aaaaattttt ttgttttttt

50

<210> 375

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (376 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44921986

<400> 375

attttttttc ttaaaaaaat ttttttgttt tttttaatac tcagaggaga g

51

<210> 376

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (375 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44921986

<400> 376

attttttttc ttaaaaaaat ttttttgttt ttttaatact cagaggagag

50

<210> 377

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (378 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44921986

<400> 377
tttttttctt aaaaaaatTT ttttgTTTT ttttaactc agaggagagg g 51

<210> 378
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (377 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44921986

<400> 378
tttttttctt aaaaaaatTT ttttgTTTT ttaactca gaggagagg 50

<210> 379
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (380 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44921986

<400> 379
cttaaaaaa ttttttTgtt ttttttaata ctCagaggag agggacatag g 51

<210> 380
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg44921986

<400> 380
cttaaaaaaa tttttttgtt tttttaatac tcagaggaga gggacatagg 50

<210> 381
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (382 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44922032

<400> 381
acgtggagac catcctgggc ctcacaggag cgaccatggg aagcctcatc t 51

<210> 382
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (381 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44922032

<400> 382
acgtggagac catcctgggc ctcacgggag cgaccatggg aagcctcatc t 51

<210> 383
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (384 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44922119

<400> 383
cagcccaggc ccagtatgat accccgaaag ctgggaagcc aggtctacct g 51

<210> 384

<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (383 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44922119

<400> 384
cagcccaggc ccagtatgat accccaaaag ctgggaagcc aggtctacct g 51

<210> 385
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (386 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44922119

<400> 385
aagcatcggt ttaaagcaca tggccttttt tttttaatta ttagtggtag 50

<210> 386
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (385 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44922119

<400> 386
aagcatcggt ttaaagcaca tggccttttt tttttaatt attagtggtg g 51

<210> 387
<211> 51
<212> DNA

<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (388 is other entry)

<221> misc_feature
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<223> Accession number cg44922119

<400> 387
tttaaagcac atggcctttt tttttaatt attagtggta gtaatatata g 51

<210> 388
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (387 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44922119

<400> 388
tttaaagcac atggcctttt tttttaatta ttagtggtag taatatatag 50

<210> 389
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (390 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44922119

<400> 389
atgtggtgac tgaggtagac gaaactacta atcttgccat cttgctttaa g 51

<210> 390
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (389 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44922119

<400> 390
atgtggtgac tgaggtacag gaaaccacta atcttgccat cttgctttaa g 51

<210> 391
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (392 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44922173

<400> 391
tggctataaaa ttctcaatta tgatacgaac atttatttta caaattctac a 51

<210> 392
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (391 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44922173

<400> 392
tggctataaaa ttctcaatta tgatatgaac atttatttta caaattctac a 51

<210> 393
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (394 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg44923068

<400> 393
ataaaaaccg gcacagcccg tctggcatgt ttgattatga ctttgagatt g 51

<210> 394
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (393 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44923068

<400> 394
ataaaaaccg gcacagcccg tctgggatgt ttgattatga ctttgagatt g 51

<210> 395
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (396 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44923491

<400> 395
gtaagcagag gtaccaaaga aagtactggg aggtgcagac tttgttaaaa g 51

<210> 396
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (395 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44923491

<400> 396
gtaagcagag gtaccaaaga aagtattggg aggtgcagac tttgttaaaa g 51

<210> 397
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (398 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44923661

<400> 397
atcacttagg accatcaaaa aaatgtgtac ctttctccaa acgacaactg a 51

<210> 398
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (397 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44923661

<400> 398
atcacttagg accatcaaaa aaatgcgtac ctttctccaa acgacaactg a 51

<210> 399
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (400 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44923666

<400> 399
attggtagca tgggttcact tggctacaac tgagcaaaat agatgcaact t 51

<210> 400
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (399 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44923666

<400> 400
attggttagca tgggttcact tggctgcaac tgagcaaat agatgcaact t 51

<210> 401
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (402 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44923675

<400> 401
aagatttgaa gcaattggtg gagtcaacag aatgggaggt tagagaaaga t 51

<210> 402
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (401 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44923675

<400> 402
aagatttgaa gcaattggtg gagtcgacag aatgggaggt tagagaaaga t 51

<210> 403
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (404 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg44923675

<400> 403

gagattaagt acaaagtgag gaagatggaa gatgggtgaa tagtgctgaa t

51

<210> 404

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (403 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44923675

<400> 404

gagattaagt acaaagtgag gaagacggaa gatgggtgaa tagtgctgaa t

51

<210> 405

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (406 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44923758

<400> 405

acttaaataa cgccatgttt aatactgaca attatttgct aaccttaaga c

51

<210> 406

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (405 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44923758

<400> 406

acttaaataa cgccatgttt aatacagaca attatttgct aaccttaaga c

51

<210> 407

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (408 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44923987

<400> 407
ccactctttg gagaccatta tgatactatg accagagtac aggcaaaagg c 51

<210> 408
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (407 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44923987

<400> 408
ccactctttg gagaccatta tgatattatg accagagtac aggcaaaagg c 51

<210> 409
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (410 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924189

<400> 409
aggatgcact gagtcagagc taaggaggagg tggacaagcg ctgaactctg c 51

<210> 410
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 2 of 2 allelic variants (409 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924189

<400> 410
aggatgcact gagtcagagc taaggaaggg tggacaagcg ctgaactctg c 51

<210> 411
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (412 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924398

<400> 411
ctgaggagcc aggagacagg ggaccggcca agggtcaccg gcaatcacat c 51

<210> 412
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (411 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924398

<400> 412
ctgaggagcc aggagacagg ggaccgcca agggtcaccg gcaatcacat c 51

<210> 413
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (414 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924398

<400> 413
agacagggga ccgccaagg gtcacggga atcacatcct taaagctgcc g 51

<210> 414
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (413 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924398

<400> 414
agacagggga ccgccaagg gtcacggga atcacatcct taaagctgcc g 51

<210> 415
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (416 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924398

<400> 415
gacaggggac attctctctc ctcacgggtg aggacagtta tcccaccagg t 51

<210> 416
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (415 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924398

<400> 416
gacaggggac attctctctc ctcacgggtg aggacagtta tcccaccagg t 51

<210> 417
<211> 51

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (418 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924574

<400> 417
aagacgaact gatccagccc cagctcggag agctctcagg agagaagctt c 51

<210> 418
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (417 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924574

<400> 418
aagacgaact gatccagccc cagcttggag agctctcagg agagaagctt c 51

<210> 419
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (420 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924623

<400> 419
gtgctgagat tacaggcatg aaccactgcc cttggacaag gcagggtttt a 51

<210> 420
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 2 of 2 allelic variants (419 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44924623

<400> 420

gtgctgagat tacaggcatg aaccattgcc cttggacaag gcagggtttt a

51

<210> 421

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (422 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44924630

<400> 421

gcttttgggt gaagggtgat ttctactaga cacatctgtg cttcagtcac a

51

<210> 422

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (421 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44924630

<400> 422

gcttttgggt gaagggtgat ttctattaga cacatctgtg cttcagtcac a

51

<210> 423

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (424 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44924824

<400> 423
ggggaggctg gagagtctgg gtggataccc tctcaatagc ccattccaag g 51

<210> 424
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (423 is other entry)

<221> misc_feature
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<223> Accession number cg44924824

<400> 424
ggggaggctg gagagtctgg gtggacaccc tctcaatagc ccattccaag g 51

<210> 425
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (426 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924824

<400> 425
ccctctcaat agccattcc aaggctactt atgaagctca taaggaatac c 51

<210> 426
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (425 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924824

<400> 426
ccctctcaat agccattcc aagggtactt atgaagctca taaggaatac c 51

<210> 427
<211> 51
<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (428 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924824

<400> 427
cccattccaa ggtcacttat gaagtcata aggaatacct agccaaaatg t 51

<210> 428
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (427 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924824

<400> 428
cccattccaa ggtcacttat gaagcacata aggaatacct agccaaaatg t 51

<210> 429
<211> 51
<212> DNA
<213> Homo sapiens

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<221> misc_feature
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<223> 1 of 2 allelic variants (430 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924824

<400> 429
cttatgaagc tcataaggaa tacctagcca aaatgtatga ggaatatcaa a 51

<210> 430
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (429 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924824

<400> 430
cttatgaagc tcataaggaa tacctggcca aaatgtatga ggaatatcaa a 51

<210> 431
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (432 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924824

<400> 431
ggaatgtgag caccatctct ggtctttcat cacagacaac aggagcaaaa g 51

<210> 432
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (431 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924824

<400> 432
ggaatgtgag caccatctct ggtctctcat cacagacaac aggagcaaaa g 51

<210> 433
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (434 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924961

<400> 433

aactcctggc ctcaagctat cctcccgct cagcctccca aagtgctgag a

51

<210> 434

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (433 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44924961

<400> 434

aactcctggc ctcaagctat cctcctgcct cagcctccca aagtgctgag a

51

<210> 435

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (436 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44925079

<400> 435

cttgggctcc cccttcattg cctctgcacc tccacactcc caaccactga c

51

<210> 436

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (435 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44925079

<400> 436

cttgggctcc cccttcattg cctctacacc tccacactcc caaccactga c

51

<210> 437

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (438 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925235

<400> 437
tcgtgttaaa ctgatgtggc agtaaacc aa gggactaagc acatgattat t 51

<210> 438
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (437 is other entry)

<221> misc_feature
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<223> Accession number cg44925235

<400> 438
tcgtgttaaa ctgatgtggc agtaatccaa gggactaagc acatgattat t 51

<210> 439
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (440 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925358

<400> 439
cggaactcgc tatatgcacg tgtgtgtgtc cgtatgtaag aaagtgtgca c 51

<210> 440
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (439 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925358

<400> 440
cggaactgc tatatgcacg tgtgtatgtc cgtatgtaag aaagtgtgca c 51

<210> 441
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (442 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925402

<400> 441
acagaagatg ctaggtttgc acgctgatga gatcctggct aacactgctg c 51

<210> 442
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (441 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925402

<400> 442
acagaagatg ctaggtttgc acgctaata ga gatcctggct aacactgctg c 51

<210> 443
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (444 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925402

<400> 443
ttcaagactt cgagtttagac agaaaccag ggggctgcgg ctctggtggt t 51

<210> 444
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (443 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925402

<400> 444
ttcaagactt cgagtttagac agaaatccag ggggctgcgg ctctggtggt t 51

<210> 445
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (446 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925406

<400> 445
aaagagccaa ggcgctggac cagtccgaca acgatatgtc cgccgtgtac c 51

<210> 446
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (445 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925406

<400> 446
aaagagccaa ggcgctggac cagtctgaca acgatatgtc cgccgtgtac c 51

<210> 447
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (448 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925534

<400> 447
cttctataac ttacttgcca ctgccttttt tttttgatag aatcttgctc t 51

<210> 448
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (447 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925534

<400> 448
cttctataac ttacttgcca ctgccttttt ttttgataga atcttgctct 50

<210> 449
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (450 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925534

<400> 449
ttgccactgc cttttttttt tgatagaatc ttgctctgctc gcccagggtg g 51

<210> 450
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (449 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925534

<400> 450
ttgccactgc cttttttttt tgataaaatc ttgctctgtc gccagggtg g 51

<210> 451
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (452 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925849

<400> 451
gaatgccact tggatgacag ttctccctaa gacccccctt tcagcatggt t 51

<210> 452
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (451 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925849

<400> 452
gaatgccact tggatgacag ttctctctaa gacccccctt tcagcatggt t 51

<210> 453
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (454 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925849

<400> 453
gctggtgtcc tcctttggga tactctcacc ccttggttcc tcagatgaaa g 51

<210> 454
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (453 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44925849

<400> 454
gctggtgtcc tcctttggga tactcccacc ccttggttcc tcagatgaaa g 51

<210> 455
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (456 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44926335

<400> 455
cacacacaca cacacacaca cacaccctta cacgaatggt aatgaaatga 50

<210> 456
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (455 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44926335

<400> 456

cacacacaca cacacacaca cacacacctt acacgaatgg taatgaaatg a

51

<210> 457

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (458 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44927187

<400> 457

ggctggggggg ctaagaagga gatcttgaga aggatggacc tgagctaaag a

51

<210> 458

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (457 is other entry)

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<222> (0)...(0)

<223> Accession number cg44927187

<400> 458

ggctggggggg ctaagaagga gatctcgaga aggatggacc tgagctaaag a

51

<210> 459

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (460 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44927553

<400> 459

actacaggca tgcaccacca caccagcta atttttgtat ttttagtaga g

51

<210> 460

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (459 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44927553

<400> 460
actacaggca tgcaccacca caccgggcta atttttgtat ttttagtaga g 51

<210> 461
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (462 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44927553

<400> 461
caccagcta atttttgtat ttttagtaga gacgggggtt catcatgttg g 51

<210> 462
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (461 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44927553

<400> 462
caccagcta atttttgtat ttttaataga gacgggggtt catcatgttg g 51

<210> 463
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (464 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44927553

<400> 463
accagctaa tttttgtatt tttagtagag acgggggtttc atcatgttg c 51

<210> 464
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (463 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44927553

<400> 464
accagctaa tttttgtatt tttagagaga cgggggtttca tcatgttggc 50

<210> 465
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (466 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44927553

<400> 465
acgggggtttc atcatgttg ccaggctggt ctcaaactcc tgacctcatg a 51

<210> 466
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (465 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg44927553

<400> 466

acggggtttc atcatgttgg ccaggttggt ctcaaactcc tgacctcatg a

51

<210> 467

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (468 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44928037

<400> 467

aaaaaagaaa agaaaagcaa aaaagaaaaa aaaaaggatt gggtagggggg a

51

<210> 468

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (467 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44928037

<400> 468

aaaaaagaaa agaaaagcaa aaaagaaaaa aaaaggattg ggtggggggga

50

<210> 469

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (470 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44928037

<400> 469
aagaaaagca aaaaagaaaa aaaaaaggat tgggtggggg gaaggaggtg g 51

<210> 470
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (469 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928037

<400> 470
aagaaaagca aaaaagaaaa aaaaaggatt ggggtggggg aaggaggtgg 50

<210> 471
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (472 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928037

<400> 471
tagatttcaa agatgaacct ggctctccat cactgagcca gacattcatt c 51

<210> 472
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (471 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928037

<400> 472
tagatttcaa agatgaacct ggctcccat cactgagcca gacattcatt c 51

<210> 473
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (474 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928115

<400> 473
catggtgact caagcctgta atcccagcac tttgggaggc cgaggcgggc g 51

<210> 474
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (473 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928115

<400> 474
catggtgact caagcctgta atcccggcac tttgggaggc cgaggcgggc g 51

<210> 475
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (476 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928274

<400> 475
tgcagtgcac acgtggtatg catgtccggc attgatcaag tccatctggg c 51

<210> 476
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (475 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928274

<400> 476
tgcagtgcac acgtggtatg catgttcggc attgatcaag tccatctggg c 51

<210> 477
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (478 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928274

<400> 477
gtccggcatt gatcaagtcc atctgggcta tggccataag ccaacaccag t 51

<210> 478
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (477 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928274

<400> 478
gtccggcatt gatcaagtcc atctgagcta tggccataag ccaacaccag t 51

<210> 479
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (480 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44928274

<400> 479

gcagagtaag tcctaaatcc atgcagcacg cagcctgagt gagatcgcca t

51

<210> 480

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (479 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44928274

<400> 480

gcagagtaag tcctaaatcc atgcaacacg cagcctgagt gagatcgcca t

51

<210> 481

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (482 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44928274

<400> 481

agacctcgaa gctggccaac atgggtagca aggggaagat catcagcggc a

51

<210> 482

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (481 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44928274

<400> 482

agacctcgaa gctggccaac atgggcagca aggggaagat catcagcggc a

51

<210> 483
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (484 is other entry)

<221> misc_feature
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<223> Accession number cg44928274

<400> 483
aagatcatca ggggcagcag cggcagcctg ctgtcttcag gttctcagga a

51

<210> 484
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (483 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928274

<400> 484
aagatcatca ggggcagcag cggcacctgc tgtcttcagg ttctcaggaa

50

<210> 485
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (486 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928329

<400> 485

ttaagaagtg taaaaaaca caacgaaaaa aaaccccaaa tcatggagaa

50

<210> 486

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (485 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44928329

<400> 486

ttaagaagtg taaaaaaca caacgaaaaa aaaaccccaa atcatggaga a

51

<210> 487

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (488 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44928356

<400> 487

ccccaacgtg tacaagaaat ccaggaggaa aggccgtcaa ggtaaaaaat g

51

<210> 488

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (487 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44928356

<400> 488

ccccaacgtg tacaagaaat ccagggggaa aggccgtcaa ggtaaaaaat g

51

<210> 489

<211> 51

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (490 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928356

<400> 489
caacgtgtac aagaaatcca ggaggaaagg ccgtcaaggt aaaaaatgga a 51

<210> 490
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (489 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928356

<400> 490
caacgtgtac aagaaatcca ggagggaagg ccgtcaaggt aaaaaatgga a 51

<210> 491
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (492 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928356

<400> 491
gtcaaggtaa aaaatggaaa ttccctctgt tccaacgctg attgagtctg t 51

<210> 492
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (491 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928356

<400> 492
gtcaaggtaa aaaatggaaa ttcccgctgt tccaacgctg attgagtctg t 51

<210> 493
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (494 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928356

<400> 493
atggaaattc cctctgttcc aacgctgatt gagtctgttg tcttaaaaga g 51

<210> 494
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (493 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928356

<400> 494
atggaaattc cctctgttcc aacgccgatt gagtctgttg tcttaaaaga g 51

<210> 495
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (496 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928356

<400> 495
gaaattccct ctgttccaac gctgattgag tctgttgtct taaaagagct t 51

<210> 496
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (495 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928356

<400> 496
gaaattccct ctgttccaac gctgactgag tctgttgtct taaaagagct t 51

<210> 497
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (498 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928356

<400> 497
gttccaacgc tgattgagtc tgttgtctta aaagagcttt aaagggcccc c 51

<210> 498
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (497 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928356

<400> 498
gttccaacgc tgattgagtc tgttgtctta aaagagcttt aaagggcccc c 51

<210> 499
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (500 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928356

<400> 499
ctgattgagt ctgttgcttt aaaagagctt taaagggcc cccttctttt c 51

<210> 500
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (499 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928356

<400> 500
ctgattgagt ctgttgcttt aaaagggtt taaagggcc cccttctttt c 51

<210> 501
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (502 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928356

<400> 501
agggccccc ttcttttcca gcactaccac tgccattcc agtcttgggt g 51

<210> 502
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (501 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg44928356

<400> 502
agggcccccc ttcttttcca gcactccac tgccattcc agtcttggt g 51

<210> 503
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (504 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928665

<400> 503
caaagccaaa cttgcaccaa aaaaagggtc atggctactg tcgggtggtc t 51

<210> 504
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (503 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928665

<400> 504
caaagccaaa cttgcaccaa aaaaagggtca tggtcactgt tcgggtggtct 50

<210> 505
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (506 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928771

<400> 505
agctggccag gcacttaatt tggggaaaga gaaggatttt gaggtaaact a 51

<210> 506
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (505 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44928771

<400> 506
agctggccag gcacttaatt tgggggaaga gaaggatttt gaggtaaact a 51

<210> 507
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (508 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44929331

<400> 507
gatgacagca actataaagg agagaagttt tcgttgaagt acactggaaa t 51

<210> 508
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (507 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44929331

<400> 508
gatgacagca actataaagg agagaggttt tcgttgaagt acactggaaa t 51

<210> 509
<211> 51

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (510 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44930314

<400> 509
tgggcgtgtc ggtggtgacg caccctgggg gctgccgggg ccatgaggtg g 51

<210> 510
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (509 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44930314

<400> 510
tgggcgtgtc ggtggtgacg caccctgggg gctgccgggg ccatgaggtg g 51

<210> 511
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (512 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44930892

<400> 511
gtgtacatat tccttgcat ttttttagtt gttgtcttaa aaaaaaaaaa a 51

<210> 512
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 2 of 2 allelic variants (511 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44930892

<400> 512

gtgtacatat tccttgcat ttttttagttg ttgtcttaaa aaaaaaaaaa

50

<210> 513

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (514 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44931317

<400> 513

aaaagttag tagagacatg gaagacgtaa aggggacccc aagcaagcct c

51

<210> 514

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (513 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44931317

<400> 514

aaaagttag tagagacatg gaagatgtaa aggggacccc aagcaagcct c

51

<210> 515

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (516 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44931528

<400> 515
tctaccagct gctcatagtc ctcacatag gtaacatagg gaatctggaa g 51

<210> 516
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (515 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44931528

<400> 516
tctaccagct gctcatagtc ctcacatag gtaacatagg gaatctggaa g 51

<210> 517
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (518 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932156

<400> 517
gcgcggcagc cccaggtcc cggggggcct cgtcacaggc tgtaggccgt g 51

<210> 518
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (517 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932156

<400> 518
gcgcggcagc cccaggtcc cgggggcct cgtcacaggc tgtaggccgt g 51

<210> 519
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (520 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 519
atgtcacatt aaaagtgcac catcgacact caatagagat taggttttac c

51

<210> 520
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (519 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 520
atgtcacatt aaaagtgcac catcggcact caatagagat taggttttac c

51

<210> 521
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (522 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 521
attcttggca gatgctgcag ataacgtgga gagcatacga aaggcacatg t

51

<210> 522
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (521 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 522
attcttggca gatgctgcag ataacatgga gagcatacga aaggcacatg t 51

<210> 523
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (524 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 523
agataacgtg gagagcatac gaaaggcaca tgtttgaacc aatagtgaca t 51

<210> 524
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (523 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 524
agataacgtg gagagcatac gaaagacaca tgtttgaacc aatagtgaca t 51

<210> 525
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (526 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg44932430

<400> 525
taacgtggag agcatacgaa aggcacatgt ttgaaccaat agtgacatac a 51

<210> 526
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (525 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 526
taacgtggag agcatacgaa aggcacatgt ttgaaccaat agtgacatac a 51

<210> 527
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (528 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 527
gagagcatac gaaaggcaca tgtttgaacc aatagtgaca tacaggtgct a 51

<210> 528
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (527 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 528
gagagcatac gaaaggcaca tgttttaacc aatagtgaca tacaggtgct a 51

<210> 529
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (530 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 529
cgaaaggcac atgtttgaac caatagtgac atacaggtgc taagttctgc a 51

<210> 530
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (529 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 530
cgaaaggcac atgtttgaac caatactgac atacaggtgc taagttctgc a 51

<210> 531
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (532 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 531
atgtttgaac caatagtgac atacaggtgc taagttctgc agtaggggaa g 51

<210> 532
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (531 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 532
atgtttgaac caatagtgac atacaagtgc taagttctgc agtaggggaa g 51

<210> 533
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (534 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 533
tgtttgaacc aatagtgaca tacaggtgct aagttctgca gtaggggaag g 51

<210> 534
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (533 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 534
tgtttgaacc aatagtgaca tacagatgct aagttctgca gtaggggaag g 51

<210> 535
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (536 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg44932430

<400> 535
tgacatacag gtgctaagtt ctgcagtagg ggaagggcag agagccatgg a 51

<210> 536
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (535 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 536
tgacatacag gtgctaagtt ctgcattagg ggaagggcag agagccatgg a 51

<210> 537
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (538 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 537
agcctcagaa aaaagttccc gttgaattgc tgttttagct gagacttgtg g 51

<210> 538
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (537 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 538
agcctcagaa aaaagttccc gttgatttgc tgttttagct gagacttgtg g 51

<210> 539

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (540 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 539
ggtagtagtt ggagatccca gacaggaggt gaccgagtta gccagggaaa a

51

<210> 540
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (539 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 540
ggtagtagtt ggagatccca gacagcaggt gaccgagtta gccagggaaa a

51

<210> 541
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (542 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 541
tcctggcacc catggcagag ttgagtgatc cagtctttct gtctctcttg g

51

<210> 542
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 2 of 2 allelic variants (541 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 542
tcctggcacc catggcagag ttgagcgatc cagtctttct gtctcctctg g 51

<210> 543
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (544 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 543
cagatctggg aatgtccagt tgggggaggg ggctgacaat gatcatgacc t 51

<210> 544
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (543 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932430

<400> 544
cagatctggg aatgtccagt tggggaaggg ggctgacaat gatcatgacc t 51

<210> 545
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (546 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932719

<400> 545
taggccttgt tcctcttcca gggaaaaaaaa gccaaatcct tatcaaggaa a 51

<210> 546
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (545 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44932719

<400> 546
taggccttgt tcctcttcca gggaagaaaa gccaaatcct tatcaaggaa a 51

<210> 547
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (548 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44938377

<400> 547
tcaaaatgtc aaaagactca gagccggggg gcaccagtgc agtgactgcg g 51

<210> 548
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (547 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44938377

<400> 548
tcaaaatgtc aaaagactca gagccagggg gcaccagtgc agtgactgcg g 51

<210> 549
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (550 is other entry)

<221> misc_feature
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<223> Accession number cg44938377

<400> 549
actcagagcc ggggggcacc agtgcagtga ctgcggattc atgggaaatg a 51

<210> 550
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (549 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44938377

<400> 550
actcagagcc ggggggcacc agtgcggtga ctgcggattc atgggaaatg a 51

<210> 551
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (552 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44938828

<400> 551
cacctcctgg tgagtaaattg tgtaaacgcg tgaagggtca gggatgtggt t 51

<210> 552
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (551 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44938828

<400> 552

cacctcctgg tgagtaaatg tgtaagcgcg tgaagggtca gggatgtgtt t

51

<210> 553

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (554 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44938869

<400> 553

taatttggtg taataaaaaat gatgcaaaaa aaaaaaaaaat cagggttggtt t

51

<210> 554

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

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<221> misc_feature

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<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44938869

<400> 554

taatttggtg taataaaaaat gatgcaaaaa aaaaaaaatc agggttggtt

50

<210> 555

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (556 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44938869

<400> 555
ataaaaaatga tgcaaaaaaaa aaaaaaatca gggttgtttg acaccttttt t 51

<210> 556
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (555 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44938869

<400> 556
ataaaaaatga tgcaaaaaaaa aaaaaatcag ggttggttga cacctttttt 50

<210> 557
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> 1 of 2 allelic variants (558 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44938869

<400> 557
taaaaaatgat gcaaaaaaaa aaaaaatcag ggttggttga cacctttttt c 51

<210> 558
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (557 is other entry)

<221> misc_feature
<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44938869

<400> 558

taaaaatgat gcaaaaaaaaa aaaaatcagg gttgtttgac accttttttc

50

<210> 559

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (560 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44938869

<400> 559

aaaccttcac caaaagggga taaaagattt aaaggcaaaa tgagtaaaca a

51

<210> 560

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (559 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44938869

<400> 560

aaaccttcac caaaagggga taaaaaattt aaaggcaaaa tgagtaaaca a

51

<210> 561

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (562 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44939935

<400> 561
acagtgtggc ctcacaggta tggcagcgga agcagctccg gtggaagaaa t 51

<210> 562
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (561 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44939935

<400> 562
acagtgtggc ctcacaggta tggcaacgga agcagctccg gtggaagaaa t 51

<210> 563
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (564 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44939935

<400> 563
cccacaaagt gcacacaggt ccccagcacc ggctcctgg tgttgggatg g 51

<210> 564
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (563 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44939935

<400> 564
cccacaaagt gcacacaggt ccccaacacc ggctcctgg tgttgggatg g 51

<210> 565
<211> 44
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (19)...(0)

<223> 1 of 2 allelic variants (566 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44939948

<400> 565

ntgcagcgga ggagagaggg ggggccaccg tggggcggtc gcac

44

<210> 566

<211> 44

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (19)...(0)

<223> 2 of 2 allelic variants (565 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44939948

<400> 566

ntgcagcgga ggagagagtg ggggccaccg tggggcggtc gcac

44

<210> 567

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (568 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44963511

<400> 567

tgtgtcttta ggctgaggca gtgcccata gctgcagtgcc tcgagtttcc g

51

<210> 568

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (567 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44963511

<400> 568
tgtgtcttta ggctgaggca gtgccatagc tgcagtgcct cgagtttccg 50

<210> 569
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (570 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44963787

<400> 569
tggtaagggg atttttgtat aagtcaatta gttgttgaat cattttctca t 51

<210> 570
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (569 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44963787

<400> 570
tggtaagggg atttttgtat aagtcattag ttgttgaatc attttctcat 50

<210> 571
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 1 of 2 allelic variants (572 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44963787

<400> 571
caggattcta tgaattaatt tttaagtagc ttagtatcat tcaatagtat t 51

<210> 572
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (571 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44963787

<400> 572
caggattcta tgaattaatt tttaactagc ttagtatcat tcaatagtat t 51

<210> 573
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (574 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44963787

<400> 573
aataccaggt tacttatact acctattcat gtagacatt tgtgtagta t 51

<210> 574
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (573 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44963787

<400> 574
aataccaggt tacttatact acctactcat gtatgacatt tgtgttagta t 51

<210> 575
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (576 is other entry)

<221> misc_feature
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<223> Accession number cg44963787

<400> 575
tcatcaaagg ggctatgagc tagacctgca gattaacacg cagatgtggc c 51

<210> 576
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (575 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44963787

<400> 576
tcatcaaagg ggctatgagc tagactgcag attaacacgc agatgtggcc 50

<210> 577
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (578 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44963787

<400> 577

cacgcagatg tggccttaaa aaaaaatcag ttaatctggg atccagagaa g 51

<210> 578
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (577 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44963787

<400> 578
cacgcagatg tggccttaaa aaaaaatcagt taatctggga tccagagaag 50

<210> 579
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (580 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44964193

<400> 579
ccttagcctt ccataatgga gaagtcgggc aggggatgtc tgcatgcaat a 51

<210> 580
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (579 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44964193

<400> 580
ccttagcctt ccataatgga gaagttgggc aggggatgtc tgcatgcaat a 51

<210> 581
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (582 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44964193

<400> 581
gggcagggga tgtctgcatg caatagacaa ctgaattaga aagagcagaa a

51

<210> 582
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (581 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44964193

<400> 582
gggcagggga tgtctgcatg caataaacia ctgaattaga aagagcagaa a

51

<210> 583
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (584 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44964193

<400> 583
ttagaaagag cagaaatgta aaccagcagt gcttcctat cttgggcctg g

51

<210> 584
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (583 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44964193

<400> 584
ttagaaagag cagaaatgta aaccaacagt gcttcctat cttgggectg g 51

<210> 585
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (586 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44965051

<400> 585
tgtccaaca ttactggct ttgggtccag tggcacagat gcagcatcag a 51

<210> 586
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (585 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44965051

<400> 586
tgtccaaca ttactggct ttgggccag tggcacagat gcagcatcag a 51

<210> 587
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (588 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg44965051

<400> 587

tgggtccagt ggcacagatg cagcatcaga accctccctc ccatacctcaa g

51

<210> 588

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (587 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44965051

<400> 588

tgggtccagt ggcacagatg cagcagcaga accctccctc ccatacctcaa g

51

<210> 589

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (590 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44965597

<400> 589

cctgacctta acctatatac tgatggaagt tcatttgtgg agaatgggat a

51

<210> 590

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (589 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44965597

<400> 590

cctgacctta acctatatac tgatgaaagt tcatttgtgg agaatgggat a

51

<210> 591

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (592 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44965597

<400> 591
ggatacaaag ggcaggttat gccatagtta gtgatgtaac cataactgaa a

51

<210> 592
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (591 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44965597

<400> 592
ggatacaaag ggcaggttat gccatgggta gtgatgtaac cataactgaa a

51

<210> 593
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (594 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44965597

<400> 593
ccccagggac cagtgccag ttagcggaac tagtggcact taccgagcc t

51

<210> 594
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 2 of 2 allelic variants (593 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44965597

<400> 594
ccccaggagac cagtgccagc ttagcagaac tagtggcact taccgagcc t 51

<210> 595
<211> 45
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (20)...(0)
<223> 1 of 2 allelic variants (596 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg5621185

<400> 595
tcctaggatt gctagcgcag caaacgccat tgttgagag cttgt 45

<210> 596
<211> 44
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (20)...(0)
<223> 2 of 2 allelic variants (595 is other entry)

<221> misc_feature
<222> (19)...(20)
<223> Nucleotide deleted between bases 19 and 20

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg5621185

<400> 596
tcctaggatt gctagcgcac aaacgccatt gtttgagagc ttgt 44

<210> 597
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (598 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg5738781

<400> 597
aatagaaagg tatgagtctc aggacggggtt ctctgcaaag cagccatcgg c 51

<210> 598
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (597 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg5738781

<400> 598
aatagaaagg tatgagtctc aggactgggtt ctctgcaaag cagccatcgg c 51

<210> 599
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (600 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg6370826

<400> 599
gttctcttct tttgtctttt ttttttcttt agagacgggg tctagctatg t 51

<210> 600
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (599 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg6370826

<400> 600
gttctcttct tttgtctttt tttttcttta gagacggggg ctagctatgt 50

<210> 601
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (602 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg6586279

<400> 601
gcgggaatgt gactgagggg cagggcccag cggctccctg cagccatcag g 51

<210> 602
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (601 is other entry)

<221> misc_feature
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<221> misc_feature
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<223> Accession number cg6586279

<400> 602
gcgggaatgt gactgagggg cagggccagc ggctccctgc agccatcagg 50

<210> 603
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (604 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg8754307

<400> 603
ttgtatgcta gggctttcaa ggggccttcg gagtggctgt tgattgtagc a 51

<210> 604
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (603 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg8754307

<400> 604
ttgtatgcta gggctttcaa ggggccttcg agtggctgtt gattgtagca 50

<210> 605
<211> 51
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<223> 1 of 2 allelic variants (606 is other entry)

<221> misc_feature
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<223> Accession number cg9886159

<400> 605
aaaacatggt atatctcgat ttatcacata aagatccaca tgaattagac g 51

<210> 606
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (605 is other entry)

<221> misc_feature
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<223> Accession number cg9886159

<400> 606

aaaacatggt atatctcgat ttatctcata aagatccaca tgaattagac g 51

<210> 607
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (608 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg9886159

<400> 607
ataaagatcc acatgaatta gacgtaaaac taggtggtat cattgaaatc t 51

<210> 608
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (607 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg9886159

<400> 608
ataaagatcc acatgaatta gacgttaaac taggtggtat cattgaaatc t 51

<210> 609
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (610 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20595730

<400> 609
aaattgaaca gagagccaaa taaacatgag aaactttatt tctccaaaga c 51

<210> 610
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (609 is other entry)

<221> misc_feature
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<223> Accession number cg20595730

<400> 610
aaattgaaca gagagccaaa taaacctgag aaactttatt tctccaaaga c 51

<210> 611
<211> 51
<212> DNA
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<220>
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<221> misc_feature
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<223> Accession number cg20611295

<400> 611
agcaagggtgg acctggtgcc tgggcacacc atgccatgct ctggagccct g 51

<210> 612
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20611295

<400> 612
agcaagggtgg acctggtgcc tgggccacca tgccatgctc tggagccctg 50

<210> 613
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (614 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20614578

<400> 613
attctctggg ttggagcgtg atggcgatcat ctatggttgg ggcacactgg a 51

<210> 614
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (613 is other entry)

<221> misc_feature
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<223> Accession number cg20614578

<400> 614
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<210> 615
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (616 is other entry)

<221> misc_feature
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<223> Accession number cg20614578

<400> 615
ggagcgtgat ggcgtcatct atggttgggg cacactggac gacaagaact c 51

<210> 616
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (615 is other entry)

<221> misc_feature
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<223> Accession number cg20614578

<400> 616

ggagcgtgat ggcgtcatct atggtcgggg cacactggac gacaagaact c

51

<210> 617

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (618 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20615101

<400> 617

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51

<210> 618

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (617 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20615101

<400> 618

attattaatt tgtaatcatt ttaacggcct ttcttcact gtaaaaagg t

51

<210> 619

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (620 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20622181

<400> 619

ccatcttgat gaagagcgga cgtaccgga acaccacggc gacagccagg a

51

<210> 620

<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (619 is other entry)

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<222> (0)...(0)
<223> Accession number cg20622181

<400> 620
ccatcttgat gaagagcgga cgtacagcga acaccacggc gacagccagg a 51

<210> 621
<211> 51
<212> DNA
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<220>
<221> misc_feature
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<223> 1 of 2 allelic variants (622 is other entry)

<221> misc_feature
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<223> Accession number cg20627797

<400> 621
ccttcgttaa aactgtcagt gtgggggata ccatcggcta cggcagaaca t 51

<210> 622
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (621 is other entry)

<221> misc_feature
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<223> Accession number cg20627797

<400> 622
ccttcgttaa aactgtcagt gtgggtgata ccatcggcta cggcagaaca t 51

<210> 623
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (624 is other entry)

<221> misc_feature
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<223> Accession number cg20627797

<400> 623
ccatcggcta cggcagaaca tggacagcca gcgaaacgac aaaaatcgcc a 51

<210> 624
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (623 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20627797

<400> 624
ccatcggcta cggcagaaca tggaccgcca gcgaaacgac aaaaatcgcc a 51

<210> 625
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (626 is other entry)

<221> misc_feature
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<223> Accession number cg20628068

<400> 625
ttcgcattggc ttcgtgggag atttcagtgg catcggactt cgatgtgccc t 51

<210> 626
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (625 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20628068

<400> 626
ttcgcatggc ttctgtgggcg atttcggtgg catcggaactt cgatgtgccc t 51

<210> 627
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (628 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20628068

<400> 627
gggcgatttc agtggcatcg gacttcgatg tgccctgcgc ccacaggggt a 51

<210> 628
<211> 51
<212> DNA
<213> Homo sapiens

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<221> misc_feature
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<223> 2 of 2 allelic variants (627 is other entry)

<221> misc_feature
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<400> 628
gggcgatttc agtggcatcg gactttgatg tgccctgcgc ccacaggggt a 51

<210> 629
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (630 is other entry)

<221> misc_feature
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<400> 629
aatattctcg gtattggtca actcagcgat gaggttgctg tcttggaaga t 51

<210> 630
<211> 51

<212> DNA
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<223> 2 of 2 allelic variants (629 is other entry)

<221> misc_feature
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<223> Accession number cg20628068

<400> 630
aatattctcg gtattggtca actcaacgat gaggttgctg tctggaaga t 51

<210> 631
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (632 is other entry)

<221> misc_feature
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<223> Accession number cg20628068

<400> 631
tggccaccg agacctcgcc ggggtggcgt ctgcccaatg actcgattcc t 51

<210> 632
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (631 is other entry)

<221> misc_feature
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<223> Accession number cg20628068

<400> 632
tggccaccg agacctcgcc ggggtagcgt ctgcccaatg actcgattcc t 51

<210> 633
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (634 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20631839

<400> 633

aggtggaagc caggatggag ggcaggcctc gccttctgtc cgggatccgc c

51

<210> 634

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (633 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20631839

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aggtggaagc caggatggag ggcagccctc gccttctgtc cgggatccgc c

51

<210> 635

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (636 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20635329

<400> 635

gtgttacatc aaatgcagtt tgttcttttt acgttgctgt gttgtatttc c

51

<210> 636

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (635 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20635329

<400> 636
gtgttacatc aaatgcagtt tgttcctttt acgttgctgt gttgtatttc c 51

<210> 637
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (638 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20635664

<400> 637
ctagtgggtgc agttttgtgt gtgtgtggac gtgctggccc agtgggtgcag g 51

<210> 638
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (637 is other entry)

<221> misc_feature
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<221> misc_feature
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<223> Accession number cg20635664

<400> 638
ctagtgggtgc agttttgtgt gtgtgggacg tgctggccca gtgggtgcagg 50

<210> 639
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (640 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20636603

<400> 639
gctgtaggca caatccatgg cttttcactt gaagccaatg tggcctctga a 51

<210> 640
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (639 is other entry)

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<222> (0)...(0)
<223> Accession number cg20636603

<400> 640
gctgtaggca caatccatgg ctttttactt gaagccaatg tggcctctga a 51

<210> 641
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (642 is other entry)

<221> misc_feature
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<223> Accession number cg20638203

<400> 641
cgcatagtagt gtgtggggcg gtggccagct catcagcagg gagcgcggt c 51

<210> 642
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (641 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20638203

<400> 642
cgcatagtagt gtgtggggcg gtggcagctc atcagcaggg agcgcggtc 50

<210> 643

<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (644 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20705188

<400> 643
tccctctcttg aatctcaagg cctggcctgt ttgggggcct gtttgggctt c 51

<210> 644
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (643 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20705188

<400> 644
tccctctcttg aatctcaagg cctggcctgt ttgggggcctg tttgggcttc 50

<210> 645
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (646 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20705880

<400> 645
ccggcccggc tatcaaccag ggagggttcac tcctgtctat cccggccggc g 51

<210> 646
<211> 51
<212> DNA

<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (645 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20705880

<400> 646
ccggcccggc tatcaaccag ggaggctcat tctgtctat cccggccggc g 51

<210> 647
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (648 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20709811

<400> 647
agtggagtga tctcaactca ctgcagcctc tacctcctgg tctcaagcag t 51

<210> 648
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (647 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20709811

<400> 648
agtggagtga tctcaactca ctgcaacctc tacctcctgg tctcaagcag t 51

<210> 649
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (650 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20710663

<400> 649
caaaaaccag tgcggagacg actaccgacg tccagcacc ggctttttcc g 51

<210> 650
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (649 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20710663

<400> 650
caaaaaccag tgcggagacg actactgacg tccagcacc ggctttttcc g 51

<210> 651
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (652 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20719026

<400> 651
cgtgttcttc ccaaagcggc gggagctcca gatccatgac gaggaggtcc t 51

<210> 652
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (651 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg20719026

<400> 652
cgtgttcttc ccaaagcggc gggagtccag atccatgacg aggaggtcct 50

<210> 653
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (654 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20721343

<400> 653
gcccgcaacg tgttaggtcg ttggtatttg tgacttggtgc tcggcgcgag c 51

<210> 654
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (653 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20721343

<400> 654
gcccgcaacg tgttaggtcg ttggtgtttg tgacttggtgc tcggcgcgag c 51

<210> 655
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (656 is other entry)

<221> misc_feature
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<223> Accession number cg20721343

<400> 655
acgtgttagg tcgttggtat ttgtgacttg tgctcggcgc gagcaaacct c 51

<210> 656
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (655 is other entry)

<221> misc_feature
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<400> 656
acgtgttagg tcgttggtat ttgtggcttg tgctcggcgc gagcaaacct c 51

<210> 657
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<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (658 is other entry)

<221> misc_feature
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<223> Accession number cg20721343

<400> 657
aggtcgttgg tatttgtgac ttgtgctcgg cgcgagcaaa cctcctgcc a 51

<210> 658
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (657 is other entry)

<221> misc_feature
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<223> Accession number cg20721343

<400> 658
aggtcgttgg tatttgtgac ttgtgttcgg cgcgagcaaa cctcctgcc a 51

<210> 659
<211> 51
<212> DNA
<213> Homo sapiens

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<221> misc_feature
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<223> Accession number cg20721343

<400> 659
ggatattgtg acttgtgctc ggcgcgagca aacctcctgc caggatgacg t 51

<210> 660
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (659 is other entry)

<221> misc_feature
<222> (0)...(0)
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<400> 660
ggatattgtg acttgtgctc ggcgcaagca aacctcctgc caggatgacg t 51

<210> 661
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (662 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20721343

<400> 661
tatttgtgac ttgtgctcgg cgcgagcaaa cctcctgccca ggatgacgtg c 51

<210> 662
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (661 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20721343

<400> 662

tatttgtagac ttgtgctcgg cgcgacaaac ctctgccag gatgacgtgc

50

<210> 663

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (664 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20721343

<400> 663

ggatgacgtg ctcagcacca acacttctca cggtcgtcac cagctccgat g

51

<210> 664

<211> 51

<212> DNA

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<222> (26)...(0)

<223> 2 of 2 allelic variants (663 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20721343

<400> 664

ggatgacgtg ctcagcacca acactcctca cggtcgtcac cagctccgat g

51

<210> 665

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (666 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20723457

<400> 665
ctttgaaaat cacacacaac ccattcgggt tttctgctat ggaaaggctc t 51

<210> 666
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (665 is other entry)

<221> misc_feature
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<223> Accession number cg20723457

<400> 666
ctttgaaaat cacacacaac ccattcgggt tttctgctat ggaaaggctc t 51

<210> 667
<211> 51
<212> DNA
<213> Homo sapiens

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<221> misc_feature
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<223> Accession number cg20724478

<400> 667
gaggctgggg agctcggcct ggctgggata cgcatgtcg tcaacgccag c 51

<210> 668
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (667 is other entry)

<221> misc_feature
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<223> Accession number cg20724478

<400> 668
gaggctgggg agctcggcct ggctgagata cgcatgtcg tcaacgccag c 51

<210> 669
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (670 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20724478

<400> 669

ctggggagct cggcctggct gggatacgcg atgtcgtaa cgccagcccg t

51

<210> 670

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (669 is other entry)

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<223> Accession number cg20724478

<400> 670

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51

<210> 671

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (672 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg20724478

<400> 671

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<210> 672

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (671 is other entry)

<221> misc_feature
<222> (0)...(0)
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<400> 672
aagacgtagc ccggtggga tgtgatggcc tgagcgtcgt ctcggcgatt t 51

<210> 673
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (674 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20724478

<400> 673
gaggggtgcc cctcatcatt gatgatcgcg tacatctcgt tgccgaaatt g 51

<210> 674
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (673 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20724478

<400> 674
gaggggtgcc cctcatcatt gatgaccgcg tacatctcgt tgccgaaatt g 51

<210> 675
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (676 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20727018

<400> 675

cacgtgcaca tctgcggtga ggttgagggc tgcagtgata ttgaaagtct c 51

<210> 676
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (675 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20727018

<400> 676
cacgtgcaca tctgcggtga ggttgagggc tgcagtgata ttgaaagtct c 51

<210> 677
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (678 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20728358

<400> 677
gatgaaaccc cgtctctact aaaaatacaa aaattagccg ggtgtgatgg c 51

<210> 678
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (677 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20728358

<400> 678
gatgaaaccc cgtctctact aaaaacacaa aaattagccg ggtgtgatgg c 51

<210> 679
<211> 36
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (11)...(0)
<223> 1 of 2 allelic variants (680 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20730743

<400> 679
acgcgtactg gcggatctca gtacgataac ccacca 36

<210> 680
<211> 36
<212> DNA
<213> Homo sapiens

<220>
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<222> (11)...(0)
<223> 2 of 2 allelic variants (679 is other entry)

<221> misc_feature
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<223> Accession number cg20730743

<400> 680
acgcgtactg acggatctca gtacgataac ccacca 36

<210> 681
<211> 51
<212> DNA
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<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (682 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20730927

<400> 681
atctgaacat ctttttatcg actactggcc ccagtgaacc tatgcaacgt c 51

<210> 682
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (681 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20730927

<400> 682
atctgaacat ctttttatcg actaccggcc ccagtgaacc tatgcaacgt c 51

<210> 683
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (684 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20738127

<400> 683
tcgatgtcga agttcgcttc gatgggcccg gaggatagcg cgtcaggtgg c 51

<210> 684
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (683 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20738127

<400> 684
tcgatgtcga agttcgcttc gatggccccg gaggatagcg cgtcaggtgg c 51

<210> 685
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (686 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20744814

<400> 685
ccatggccac ccacgaagct ctccctgcc cctccgtcgc ccaactcctg g 51

<210> 686
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (685 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20744814

<400> 686
ccatggccac ccacgaagct ctccccgcc cctcgcgcg ccaactcctg g 51

<210> 687
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (688 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20744814

<400> 687
gaggggcacc cgggtgctgc tggccatggc caccacgaa gctctccctg c 51

<210> 688
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (687 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20744814

<400> 688
gaggggcacc cgggtgctgc tggcgtggc caccacgaa gctctccctg c 51

<210> 689
<211> 46
<212> DNA
<213> Homo sapiens

<220>
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<222> (21)...(0)
<223> 1 of 2 allelic variants (690 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20745811

<400> 689
nacgcgtggg gcatgtcaga gcttcagatg tgcattgcga acatgc

46

<210> 690
<211> 46
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (21)...(0)
<223> 2 of 2 allelic variants (689 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg20745811

<400> 690
nacgcgtggg gcatgtcaga acttcagatg tgcattgcga acatgc

46

<210> 691
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (692 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21132570

<400> 691
gtatgtacga gtgtgcacgt gtgtgctgt gcacagagg tgggtgccca g

51

<210> 692
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (691 is other entry)

<221> misc_feature

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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21132570

<400> 692
gtatgtacga gtgtgcacgt gtgtggtgtg cacagagggt gtggtgccag 50

<210> 693
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (694 is other entry)

<221> misc_feature
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<223> Accession number cg21132570

<400> 693
cgagtgtgca cgtgtgtgcg tgtgcacaga ggggtgtggtg ccagcttgag t 51

<210> 694
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (693 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
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<400> 694
cgagtgtgca cgtgtgtgcg tgtgccagag ggtgtggtgc cagcttgagt 50

<210> 695
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (696 is other entry)

<221> misc_feature
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<223> Accession number cg21147609

<400> 695
agtgcagagc caggatccac ctgagtcccc cggctggctc cagatccac a 51

<210> 696
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (695 is other entry)

<221> misc_feature
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<223> Accession number cg21147609

<400> 696
agtgcagagc caggatccac ctgagcccc cggctggctc cagatccac a 51

<210> 697
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (698 is other entry)

<221> misc_feature
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<223> Accession number cg21147771

<400> 697
gactggctta ttccacttag cataatgtcc tcaaggtgtg ttcacccatg t 51

<210> 698
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (697 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21147771

<400> 698

gactggctta ttccacttag cataacgtcc tcaaggtgtg ttcacccatg t

51

<210> 699

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (700 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21147771

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51

<210> 700

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (699 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21147771

<400> 700

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51

<210> 701

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (702 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21147771

<400> 701

gctggagtc agtgatgcaa tctcggctca ctgcaacctc cgctcccag c

51

<210> 702

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (701 is other entry)

<221> misc_feature
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<400> 702
gctggagtgc agtgatgcaa tctcgactca ctgcaacctc cgctcccag c 51

<210> 703
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (704 is other entry)

<221> misc_feature
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<223> Accession number cg21148047

<400> 703
tgcttatatt cctgttggtg ggaatataaa accgtacatc tagtatggaa a 51

<210> 704
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (703 is other entry)

<221> misc_feature
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<223> Accession number cg21148047

<400> 704
tgcttatatt cctgttggtg ggaatgtaaa accgtacatc tagtatggaa a 51

<210> 705
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (706 is other entry)

<221> misc_feature
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<223> Accession number cg21148047

<400> 705
attgagggat gaatggaaaa acaaaatctg acatatacat acatacagtg g 51

<210> 706
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (705 is other entry)

<221> misc_feature
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<223> Accession number cg21148047

<400> 706
attgagggat gaatggaaaa acaaagtctg acatatacat acatacagtg g 51

<210> 707
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (708 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21148047

<400> 707
catatagaca tatgctataa catggatgca ccttgagtac attatgctag g 51

<210> 708
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (707 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21148047

<400> 708
catatagaca tatgctataa catggctgca ccttgagtac attatgctag g 51

<210> 709
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (710 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21148047

<400> 709
ggatgcacct tgagtacatt atgctaggtg aaataagcct gtcacaaaaa c

51

<210> 710
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (709 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21148047

<400> 710
ggatgcacct tgagtacatt atgctgggtg aaataagcct gtcacaaaaa c

51

<210> 711
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (712 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21148047

<400> 711
tgagtacatt atgctaggtg aaataagcct gtcacaaaaa caaatactgc a

51

<210> 712
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (711 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21148047

<400> 712
tgagtacatt atgctaggtag aaataggcct gtcacaaaaa caaatactgc a 51

<210> 713
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (714 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21148047

<400> 713
aaacaaatac tgcattgattc cattttaaag aggggcctag aatattcaac t 51

<210> 714
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (713 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21148047

<400> 714
aaacaaatac tgcattgattc catttgaatg aggggcctag aatattcaac t 51

<210> 715
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (716 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21148047

<400> 715

aacaaatact gcatgattcc atttaaata ga ggggcctaga atattcaact t

51

<210> 716

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (715 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21148047

<400> 716

aacaaatact gcatgattcc atttagatga ggggcctaga atattcaact t

51

<210> 717

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (718 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21150410

<400> 717

ggcggaggtt tcagagtaga aggtgatgtc agctccagct cccctctgtc g

51

<210> 718

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (717 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21150410

<400> 718

ggcggaggtt tcagagtaga aggtggtgtc agctccagct cccctctgtc g

51

<210> 719
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (720 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21150410

<400> 719
gaataagaag atgaagtttg cagtcgaatt catgttctcc taccctgct c 51

<210> 720
<211> 51
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<220>
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<223> 2 of 2 allelic variants (719 is other entry)

<221> misc_feature
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<223> Accession number cg21150410

<400> 720
gaataagaag atgaagtttg cagtcaaatt catgttctcc taccctgct c 51

<210> 721
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (722 is other entry)

<221> misc_feature
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<223> Accession number cg21405503

<400> 721
gaaagacttc tagttcacag gggctgtatc tgaaccctaa aacaggccca g 51

<210> 722
<211> 51
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<223> 2 of 2 allelic variants (721 is other entry)

<221> misc_feature
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<223> Accession number cg21405503

<400> 722
gaaagacttc tagttcacag gggctctatc tgaaccctaa aacaggccca g 51

<210> 723
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<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (724 is other entry)

<221> misc_feature
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<223> Accession number cg21415668

<400> 723
ggactggtca gggaggagtt agggcaggag gactgggtcag ggaggagtta g 51

<210> 724
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (723 is other entry)

<221> misc_feature
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<223> Accession number cg21415668

<400> 724
ggactggtca gggaggagtt agggctggag gactgggtcag ggaggagtta g 51

<210> 725
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (726 is other entry)

<221> misc_feature
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<223> Accession number cg21415668

<400> 725

ggactggtca gggaggagtt agggcaggag gactggtcag ggaggagtta g

51

<210> 726

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (725 is other entry)

<221> misc_feature

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<223> Accession number cg21415668

<400> 726

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51

<210> 727

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (728 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21417734

<400> 727

tcttgccgt tctcgacagg agcgcatcat ggaccagccc agcaatctgt t

51

<210> 728

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (727 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21417734

<400> 728
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<210> 729
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (730 is other entry)

<221> misc_feature
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<223> Accession number cg21424662

<400> 729
tgaggaagag gaaatacaga actcagctgt cccgggggtg cgcgctgtg t 51

<210> 730
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (729 is other entry)

<221> misc_feature
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<400> 730
tgaggaagag gaaatacaga actcacctgt cccgggggtg cgcgctgtg t 51

<210> 731
<211> 51
<212> DNA
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<400> 731
gtgctgtgcc gcgagcgcg cgagggcggc gtgtgtgtgt gtgtgtgtgt g 51

<210> 732
<211> 51
<212> DNA

<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (731 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21424662

<400> 732
gtgctgtgcc gcgagcgcgc gcgagacggc gtgtgtgtgt gtgtgtgtgt g 51

<210> 733
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (734 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg21424662

<400> 733
gtgtgtgtgt gtgtgtgtgt gtgtggtgtg tgcgcgcgcg cgtatgtatg 50

<210> 734
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (733 is other entry)

<221> misc_feature
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<400> 734
gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgcgcgcgc gcgtatgtat g 51

<210> 735
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (736 is other entry)

<221> misc_feature
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<400> 735
tgtgtgtgtg tgtgtgtggt gtgtg'gcgcgc ggcgcgtatgt atgtgtgtgt g 51

<210> 736
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (735 is other entry)

<221> misc_feature
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<223> Accession number cg21424662

<400> 736
tgtgtgtgtg tgtgtgtggt gtgtgtg'gcgc ggcgcgtatgt atgtgtgtgt g 51

<210> 737
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (738 is other entry)

<221> misc_feature
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<223> Accession number cg21424863

<400> 737
ggaccgttcg cgctgcacctg ggctcgttgg agggcattat gcctccggcg g 51

<210> 738
<211> 51
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<223> 2 of 2 allelic variants (737 is other entry)

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<222> (0)...(0)
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<400> 738
ggaccgttcg cgtcgacctg ggctcattgg agggcattat gcctccggcg g 51

<210> 739
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (740 is other entry)

<221> misc_feature
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<400> 739
tcgttgagg gcattatgcc tccggcggaa caggttcccg gggagaaata t 51

<210> 740
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<400> 740
tcgttgagg gcattatgcc tccggggaac aggttcccg ggagaaatat 50

<210> 741
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (742 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21424863

<400> 741
caactgcccg gcaggtcatt ttccaacggc tgcgcgaggc cgaggacgag c 51

<210> 742
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (741 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21424863

<400> 742
caactgcccg gcaggtcatt ttccagcggc tgcgcgaggc cgaggacgag c 51

<210> 743
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (744 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21424863

<400> 743
ggacgagcag aaatacggtc atttttccgc cgttgagggt gacgtcatca c 51

<210> 744
<211> 51
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<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (743 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21424863

<400> 744
ggacgagcag aaatacggtc attttgccgc cgttgagggt gacgtcatca c 51

<210> 745
<211> 51

<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (746 is other entry)

<221> misc_feature
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agcagaaata cggtcatttt tccgccgttg agggtgacgt catcacgga g 51

<210> 746
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (745 is other entry)

<221> misc_feature
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<400> 746
agcagaaata cggtcatttt tccgccgttg agggtgacgt catcacgga g 51

<210> 747
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (748 is other entry)

<221> misc_feature
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<223> Accession number cg21424863

<400> 747
aatacggtca tttttccgcc gttgagggtg acgtcatcac cggagtcgtc c 51

<210> 748
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (747 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21424863

<400> 748

aatacgggtca tttttccgcc gttgaagggtg acgtcatcac cggagtcgtc c

51

<210> 749

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (750 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21425684

<400> 749

tgcacctgac gcggttcgac gtgcagatcg aggccttcga agagcccctc c

51

<210> 750

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (749 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21425684

<400> 750

tgcacctgac gcggttcgac gtgcatatcg aggccttcga agagcccctc c

51

<210> 751

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (752 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21425684

<400> 751
agaaggcatc cgtgaggatc cgcacagcca gggccagggc gatttccttg a 51

<210> 752
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (751 is other entry)

<221> misc_feature
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<400> 752
agaaggcatc cgtgaggatc cgcacggcca gggccagggc gatttccttg a 51

<210> 753
<211> 51
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<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (754 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21425687

<400> 753
ccccagaaga gggagggcgc tctctgccca ggagacctgc tgtgctccca t 51

<210> 754
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (753 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21425687

<400> 754
ccccagaaga gggagggcgc tctcttccca ggagacctgc tgtgctccca t 51

<210> 755
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<212> DNA

<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (756 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21428753

<400> 755
ccttcctct gtacctgtgt cctgaccccc ttttcttata aggacaccgg t 51

<210> 756
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (755 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21428753

<400> 756
ccttcctct gtacctgtgt cctgaacccc ttttcttata aggacaccgg t 51

<210> 757
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (758 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21428762

<400> 757
catcagaggt gaaaacgatg agcgggggtgc tcggacgcag acgagcgata c 51

<210> 758
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (757 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21428762

<400> 758
catcagaggt gaaaacgatg agcgggtgtgc tcggacgcag acgagcgata c 51

<210> 759
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (760 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21428762

<400> 759
acaccggggt aacgacggcg tgagcgcccc agaccaggc gagggctcttg g 51

<210> 760
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (759 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21428762

<400> 760
acaccggggt aacgacggcg tgagcccca gaccaggcg agggctcttg 50

<210> 761
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (762 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21433543

<400> 761

tacgcctccc tcaccactcc gacgcgtacc ttcgtcgtcg ccgtgacagc a

51

<210> 762

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (761 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21433543

<400> 762

tacgcctccc tcaccactcc gacgcatacc ttcgtcgtcg ccgtgacagc a

51

<210> 763

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (764 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21433543

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tccgacgcgt accttcgtcg tcgccgtgac agcagccgta tgcggggccg c

51

<210> 764

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (763 is other entry)

<221> misc_feature

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<223> Accession number cg21433543

<400> 764

tccgacgcgt accttcgtcg tcgccatgac agcagccgta tgcggggccg c

51

<210> 765
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (766 is other entry)

<221> misc_feature
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<223> Accession number cg21433543

<400> 765
cactgaagtt atggcgtcgc tgcgtagccg aggctgggggt agcgctcctg g 51

<210> 766
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (765 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21433543

<400> 766
cactgaagtt atggcgtcgc tgcgtagccg aggctgggggt agcgctcctg g 51

<210> 767
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (768 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21435343

<400> 767
cggggcctct ggctggcag ccgcaggacc caatggatcg ggcgctcacg c 51

<210> 768
<211> 50
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (767 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21435343

<400> 768
cggggcctct ggccctggcag ccgcagaccc aatggatcgg gcgctcacgc 50

<210> 769
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (770 is other entry)

<221> misc_feature
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<223> Accession number cg21435589

<400> 769
tcattttgtg ccaagataca ctgtcgggtgc ctgatccgga atgggtctgtg t 51

<210> 770
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (769 is other entry)

<221> misc_feature
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<223> Accession number cg21435589

<400> 770
tcattttgtg ccaagataca ctgtcagtgct ctgatccgga atgggtctgtg t 51

<210> 771
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (772 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21628871

<400> 771

gcccggaccc tgtaccgcga ccaggacaca gcccatcact aatcaatgat a

51

<210> 772

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (771 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21628871

<400> 772

gcccggaccc tgtaccgcga ccagggcaca gcccatcact aatcaatgat a

51

<210> 773

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (774 is other entry)

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<223> Accession number cg21628871

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ggacacagcc catcactaat caatgatatt tccataaacc aaagagaatt c

51

<210> 774

<211> 51

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<222> (26)...(0)

<223> 2 of 2 allelic variants (773 is other entry)

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<222> (0)...(0)

<223> Accession number cg21628871

<400> 774
ggacacagcc catcactaat caatggtatt tccataaacc aaagagaatt c 51

<210> 775
<211> 51
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<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (776 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21632268

<400> 775
aagaacacccc gtgacaaaag aaggagggcc ggcagaatga cccgccggcc c 51

<210> 776
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21632268

<400> 776
aagaacacccc gtgacaaaag aaggaggccg gcagaatgac cccgccggccc 50

<210> 777
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (778 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21632268

<400> 777
gacggtcgtc acttctcctc tttgggcagc cgccactggt cgtgctcggt g 51

<210> 778
<211> 50
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<400> 778
gacggtcgtc acttctcctc ttggcagcc gccactggtc gtgctcggtg

50

<210> 779
<211> 51
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<221> misc_feature
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<400> 779
gcggacgcgg gccgtgataa tcagggccgt aggctcccgg agcggggcga c

51

<210> 780
<211> 50
<212> DNA
<213> Homo sapiens

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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21632268

<400> 780
gcggacgcgg gccgtgataa tcaggccgta ggctcccga gcggggcgac 50

<210> 781
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (782 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21632288

<400> 781
gtgtgagggg cgcggcgccc cctagccggc cctgcgccgg ggtctcagag g 51

<210> 782
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (781 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21632288

<400> 782
gtgtgagggg cgcggcgccc cctagccggc cctgcgccgg ggtctcagag g 51

<210> 783
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (784 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21632288

<400> 783
gccggggtct cagagggccg gccggcggg gggcgccgg gggccaggac t 51

<210> 784
<211> 50
<212> DNA

<213> Homo sapiens

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<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21632288

<400> 784
gccgggggtct cagagggccg gccgcgggg ggcgccgcgg ggccaggact 50

<210> 785
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (786 is other entry)

<221> misc_feature
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<223> Accession number cg21632288

<400> 785
gagggccggc ccggcggggg gcgccgcggg gccaggactg cgctcaggat c 51

<210> 786
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (785 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg21632288

<400> 786
gagggccggc ccggcggggg gcgcccgggg ccaggactgc gctcaggatc 50

<210> 787

<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (788 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21634562

<400> 787
cctggctcag cagagccgcc ttctgctgc agaagctgat gtcgccccac c 51

<210> 788
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (787 is other entry)

<221> misc_feature
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<223> Accession number cg21634562

<400> 788
cctggctcag cagagccgcc ttctactgc agaagctgat gtcgccccac c 51

<210> 789
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (790 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21638303

<400> 789
caagcctggt atacaaccag atctcatgag aactcactat cacaaggtea g 51

<210> 790
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (789 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21638303

<400> 790
caagcctgtt atacaaccag atctcctgag aactcactat cacaaggcca g 51

<210> 791
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (792 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21638303

<400> 791
tgagaactca ctatcacaag gtcagcatca agaagatggt gcttaaccat t 51

<210> 792
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<221> misc_feature
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<400> 792
tgagaactca ctatcacaag gtcagtatca agaagatggt gcttaaccat t 51

<210> 793
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (794 is other entry)

<221> misc_feature
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<400> 793
tcacaaggctc agcatcaaga agatggtgct taaccattgg tgaaagatcc g 51

<210> 794
<211> 51
<212> DNA
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<400> 794
tcacaaggctc agcatcaaga agatggtgct taaccattgg tgaaagatcc g 51

<210> 795
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<220>
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<223> 1 of 2 allelic variants (796 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21638638

<400> 795
gaggaaggc ctcccatgta cccgtcactc ctctcttctc catcaaggcc a 51

<210> 796
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> 2 of 2 allelic variants (795 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21638638

<400> 796
gaggaaggc ctcccatgta cccgttactc ctctcttctc catcaaggcc a 51

<210> 797
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (798 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21639240

<400> 797
ttgccacgtt gcctaggctg gtctcaaact cctgggctca gatgatccac c 51

<210> 798
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (797 is other entry)

<221> misc_feature
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<223> Accession number cg21639240

<400> 798
ttgccacgtt gcctaggctg gtctcgaact cctgggctca gatgatccac c 51

<210> 799
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (800 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21639652

<400> 799
aaaacccatg cactcctgtg ggattgcccc tgagctccac agtctctccc c 51

<210> 800
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)

<223> 2 of 2 allelic variants (799 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21639652

<400> 800

aaaacccatg cactcctgtg ggattacccc tgagctccac agtctctccc c

51

<210> 801

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (802 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21640260

<400> 801

tgtcaccag gctgaactgc agtgggtgtga tcttggtca ctgcaacctc c

51

<210> 802

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (801 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21640260

<400> 802

tgtcaccag gctgaactgc agtggcgtga tcttggtca ctgcaacctc c

51

<210> 803

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (804 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21640260

<400> 803
tggctcactg caacctccac ctcccaggtt caagcaattc tctgcctca g 51

<210> 804
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (803 is other entry)

<221> misc_feature
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<400> 804
tggctcactg caacctccac ctcccgggtt caagcaattc tctgcctca g 51

<210> 805
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (806 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21640260

<400> 805
caacctccac ctcccaggtt caagcaattc tctgcctca gcctcagcct c 51

<210> 806
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 2 of 2 allelic variants (805 is other entry)

<221> misc_feature
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<223> Accession number cg21640260

<400> 806
caacctccac ctcccaggtt caagcgattc tctgcctca gcctcagcct c 51

<210> 807
<211> 51
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<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (808 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21642593

<400> 807

cggccacccc cgaccagcc cgcacgcca gggcgtagcc atcggtcatc g

51

<210> 808

<211> 51

<212> DNA

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<223> Accession number cg21642593

<400> 808

cggccacccc cgaccagcc cgcacaccca gggcgtagcc atcggtcatc g

51

<210> 809

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (810 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21643872

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51

<210> 810

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (809 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21643872

<400> 810
ccgaagaccc agccaagccg tccaaaatct tcgctcccag tggctcatg c 51

<210> 811
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (812 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21646394

<400> 811
aggaagcaga gtctatacaa aatttaagag aatgagacag aagacgctcc t 51

<210> 812
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (811 is other entry)

<221> misc_feature
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<223> Accession number cg21646394

<400> 812
aggaagcaga gtctatacaa aatttgagag aatgagacag aagacgctcc t 51

<210> 813
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (814 is other entry)

<221> misc_feature
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<400> 813

gcatccccgc acagcacgtg gtgtgtggac atgccacagc atccgcggga g

51

<210> 814

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (813 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21651520

<400> 814

gcatccccgc acagcacgtg gtgtgctggac atgccacagc atccgcggga g

51

<210> 815

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (816 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21652256

<400> 815

actgcagcgt gagccctggg acgcagtcga agcagagcaa agtctcccc g

51

<210> 816

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (815 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21652256

<400> 816

actgcagcgt gagccctggg acgcaatcga agcagagcaa agtctcccc g

51

<210> 817

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (818 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21655657

<400> 817
caacatacat ggcgtttgcg tcacagttgg agtcagatgt gagcccggag g 51

<210> 818
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (817 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21655657

<400> 818
caacatacat ggcgtttgcg tcacaattgg agtcagatgt gagcccggag g 51

<210> 819
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (820 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21656849

<400> 819
caccagaac cacggattac gcaacgcacg ctgccaccag ggacgacgcg c 51

<210> 820
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (819 is other entry)

<221> misc_feature
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<223> Accession number cg21656849

<400> 820
caccagaac cacggattac gcaacacacg ctgccaccag ggacgacg c 51

<210> 821
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (822 is other entry)

<221> misc_feature
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<223> Accession number cg21656849

<400> 821
aggactgggtt ggtgatcccc gggatgacac cttctgacc ttgctgctcg a 51

<210> 822
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (821 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21656849

<400> 822
aggactgggtt ggtgatcccc gggataacac cttctgacc ttgctgctcg a 51

<210> 823
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (824 is other entry)

<221> misc_feature
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<223> Accession number cg21656849

<400> 823
cgggatgaca cccttctgac cttgctgctc gacctcagta tcggcatgca c 51

<210> 824
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (823 is other entry)

<221> misc_feature
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<223> Accession number cg21656849

<400> 824
cgggatgaca cccttctgac cttgccgctc gacctcagta tcggcatgca c 51

<210> 825
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (826 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21659091

<400> 825
gttcaaacca aatcctgctc ctgaggagac agaaggggca ggacttccag a 51

<210> 826
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> 2 of 2 allelic variants (825 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21659091

<400> 826
gttcaaacca aatcctgctc ctgagtagac agaaggggca ggacttccag a 51

<210> 827
<211> 38
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (13)...(0)
<223> 1 of 2 allelic variants (828 is other entry)

<221> misc_feature
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<223> Accession number cg21659216

<400> 827
acgcgtgtgt cctgtgacta caaaacagca ctgggggtt

38

<210> 828
<211> 38
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (827 is other entry)

<221> misc_feature
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<223> Accession number cg21659216

<400> 828
acgcgtgtgt cccgtgacta caaaacagca ctgggggtt

38

<210> 829
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (830 is other entry)

<221> misc_feature
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<223> Accession number cg21659216

<400> 829
aaggatgctg ggacctggag tcaggcaagt tgcagccaag ctcagccttt g

51

<210> 830
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (829 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg21659216

<400> 830
aaggatgctg ggacctggag tcaggtaagt tgcagccaag ctcagccttt g 51

<210> 831
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<221> misc_feature
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<223> Accession number cg21659349

<400> 831
acattcgct caatggagac ccggtcaaac cctcccacgc cgtgaaaccc g 51

<210> 832
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (831 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21659349

<400> 832
acattcgct caatggagac ccggttaaac cctcccacgc cgtgaaaccc g 51

<210> 833
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<223> 1 of 2 allelic variants (834 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21659349

<400> 833
ggagaccgg tcaaaccctc ccacgccgtg aaaccggcg atacggtcac c 51

<210> 834
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (833 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21659349

<400> 834
ggagaccg tcaaaccctc ccacgacgtg aaaccggcg ataccgtcac c 51

<210> 835
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (836 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21659349

<400> 835
cgtgaaaccc ggcgataccg tcaccgtcca ccccccgga tgggaccggg t 51

<210> 836
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (835 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21659349

<400> 836
cgtgaaaccc ggcgataccg tcaccatcca ccccccgga tgggaccggg t 51

<210> 837
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (838 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21659349

<400> 837
tccacacccc cggatgggac cgggttctcc aggtcatcaa cccgatcacg a 51

<210> 838
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (837 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21659349

<400> 838
tccacacccc cggatgggac cgggtcctcc aggtcatcaa cccgatcacg a 51

<210> 839
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (840 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21660290

<400> 839
agggtggaacg ggcactggac ctgtgcatgg cgtgcaaagg gtgcgccga g 51

<210> 840
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (839 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg21660290

<400> 840

aggtggaacg ggcactggac ctgtgtatgg cgtgcaaagg gtgcgcccga g

51

<210> 841

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (842 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21660634

<400> 841

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51

<210> 842

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (841 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21660634

<400> 842

cccacaccag gaaacagata ccaatgaggg tccacgtgac gaccggaaca t

51

<210> 843

<211> 50

<212> DNA

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<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21660687

<400> 843
ctcaaccgcc tgacgcgctc gctgcccgcg cgcgccaccgt ggagttgccc 50

<210> 844
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (843 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21660687

<400> 844
ctcaaccgcc tgacgcgctc gctgcccgcg cgcgccaccg tggagttgcc c 51

<210> 845
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (846 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21660975

<400> 845
gcaggggcat tggggtaata gccttttagc cctttttgag ggaaacacat g 51

<210> 846
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (845 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg21660975

<400> 846
gcaggggcat tggggtaata gccttttagc cctttttgag ggaaacacat g 51

<210> 847
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (848 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21661807

<400> 847

tgccttcagg agcagacccc cacacgtatg agccgtcgct gcgtgacgtt c

51

<210> 848

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (847 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg21661807

<400> 848

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51

<210> 849

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (850 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg23217486

<400> 849

gctatggctg tggatttcgg agtgcgggga agtgtggagg aggtgttggg g

51

<210> 850

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (849 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg23217486

<400> 850
gctatggctg tggatttcgg agtgctggga agtggtggagg aggtgttggg g 51

<210> 851
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (852 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg23217486

<400> 851
ggatttcgga gtgcggggaa gtgtggagga ggtgttgggg gctggagaga t 51

<210> 852
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (851 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg23217486

<400> 852
ggatttcgga gtgcggggaa gtgtgcagga ggtgttgggg gctggagaga t 51

<210> 853
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (854 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg23295774

<400> 853

gccccctcctg agtgccaagg aggcggggcgt ctacacttgc cgtgcacaca a

51

<210> 854

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (853 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg23295774

<400> 854

gccccctcctg agtgccaagg aggcgagcgt ctacacttgc cgtgcacaca a

51

<210> 855

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (856 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg23295774

<400> 855

gccaaactcta cgtcaatacgt cgtggcggtg gcagcaaccg ggcccccaaa a

51

<210> 856

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (855 is other entry)

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<222> (0)...(0)

<223> Accession number cg23295774

<400> 856

gccaaactcta cgtcaatacgt cgtggaggtg gcagcaaccg ggcccccaaa a

51

<210> 857

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (858 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg23298372

<400> 857
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<210> 858
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (857 is other entry)

<221> misc_feature
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<223> Accession number cg23298372

<400> 858
cgcgtgatag gctcaggagc ctgcccgtgt acacagacag cacacatgac a 51

<210> 859
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (860 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg23298372

<400> 859
ctgtgtacac agacagcaca catgacaggc ccgggagcct gtctgtgtac a 51

<210> 860
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (859 is other entry)

<221> misc_feature
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<223> Accession number cg23298372

<400> 860
ctgtgtacac agacagcaca catgataggc cggggagcct gtctgtgtac a 51

<210> 861
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (862 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg23299043

<400> 861
agtacgacat cgcacacgct tcagaccgac cagagtgaag aatttcgcgt a 51

<210> 862
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (861 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg23299043

<400> 862
agtacgacat cgcacacgct tcagagcgac cagagtgaag aatttcgcgt a 51

<210> 863
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (864 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg23299248

<400> 863

ccaactatta agatatatat acccctaccc cagtgaagaa caatctgcta

50

<210> 864

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (863 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg23299248

<400> 864

ccaactatta agatatatat acccctacc ccagtgaaga acaatctgct a

51

<210> 865

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (866 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg23305320

<400> 865

tgctgcatac caggtgccaa atggcgctcct ataaatggaa gctcttggt g

51

<210> 866

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (865 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg23305320

<400> 866

tgctgcatac caggtgccaa atggcatcct ataaatggaa gctcttggt g

51

<210> 867

<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (868 is other entry)

<221> misc_feature
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<223> Accession number cg23306056

<400> 867
tccagtatga ctttatctcg attacacctg taaagacctt aagccatatt t 51

<210> 868
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (867 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg23306056

<400> 868
tccagtatga ctttatctcg attaccctgt aaagacctta agccatattt 50

<210> 869
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (870 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg23306056

<400> 869
actttatctc gattacacct gtaaagacct taagccatat ttttaaggttc t 51

<210> 870
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (869 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg23306056

<400> 870

actttatctc gattacacct gtaaatacct taagccatat tttaagggtc t

51

<210> 871

<211> 48

<212> DNA

<213> Homo sapiens

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<222> (23)...(0)

<223> 1 of 2 allelic variants (872 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg23309108

<400> 871

acgcgtgccc gttacgttga ccaggctggt tgtaaactcc tgggctca

48

<210> 872

<211> 48

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (23)...(0)

<223> 2 of 2 allelic variants (871 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg23309108

<400> 872

acgcgtgccc gttacgttga ccgggctggt tgtaaactcc tgggctca

48

<210> 873

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (874 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg23309108

<400> 873
tgggctcaag tgatccacct gcctcagcct ccaaaagtgc tgggattaca t 51

<210> 874
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (873 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg23309108

<400> 874
tgggctcaag tgatccacct gcctcggcct ccaaaagtgc tgggattaca t 51

<210> 875
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (876 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg23331833

<400> 875
acagcgcgta ctttgggctc cgggattcgc tccgcgcccg cggttgtagc a 51

<210> 876
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (875 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg23331833

<400> 876

acagcgcgta ctttgggctc cgggagtcgc tccgcgcccg cggttgtagc a

51

<210> 877

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (878 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg23332230

<400> 877

ttgtgggagt attaggggaa gttgccacta aggctggcag gtcttgaggt t

51

<210> 878

<211> 50

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (877 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg23332230

<400> 878

ttgtgggagt attaggggaa gttgcactaa ggctggcagg tcctggagtt

50

<210> 879

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (880 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg23333370

<400> 879

ttgggggctc agaggcacgg ttaacgcagc agcagcgcaa acctcacact c

51

<210> 880
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (879 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg23333370

<400> 880
ttgggggctc agaggcacgg ttaacacagc agcagcgcaa acctcacact c 51

<210> 881
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (882 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg24109555

<400> 881
aatataatgg gtttatatga ctatatcaaa ggagggaaga agggccccag c 51

<210> 882
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (881 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg24109555

<400> 882
aatataatgg gtttatatga ctatacaaaa ggagggaaga agggccccag c 51

<210> 883
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (884 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg24110526

<400> 883
gcactgagac agcatcacga ggactgtgcc tgccccgcat gcctcttgcc a 51

<210> 884
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (883 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg24110526

<400> 884
gcactgagac agcatcacga ggactatgcc tgccccgcat gcctcttgcc a 51

<210> 885
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (886 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg24113982

<400> 885
tacttagtta tgtttttaaa cacacatctg agtcaaagc caagaaaggg a 51

<210> 886
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (885 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg24113982

<400> 886

tacttagtta tgttttttaa cacacgtctg agtcaaagc caagaaagg a

51

<210> 887

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (888 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg24114224

<400> 887

aatgggccag gctggagcta cgttgagttt gttgagttt ttgcttattg c

51

<210> 888

<211> 51

<212> DNA

<213> Homo sapiens

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aatgggccag gctggagcta cgttgcgttt gttgagttt ttgcttattg c

51

<210> 889

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (890 is other entry)

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<223> Accession number cg24114456

<400> 889

atcctgacgt gtagactcct atggagacct acttaattca caccgggtgt c

51

<210> 890

<211> 51
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<223> 2 of 2 allelic variants (889 is other entry)

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<400> 890
atcctgacgt gtagactcct atggatacct acttaattca caccgggtgt c 51

<210> 891
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<400> 891
ttcacaccgg gtgtcctgat gtgtagaccc ctgtggagac ctacttaatt c 51

<210> 892
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<223> 2 of 2 allelic variants (891 is other entry)

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ttcacaccgg gtgtcctgat gtgtaaacc ctgtggagac ctacttaatt c 51

<210> 893
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<223> 1 of 2 allelic variants (894 is other entry)

<221> misc_feature
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<223> Accession number cg24115035

<400> 893
gaggtgaaag ggaagaaaag ctaaggtcga ccttagaaaag cattgagtca a 51

<210> 894
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (893 is other entry)

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<400> 894
gaggtgaaag ggaagaaaag ctaagatcga ccttagaaaag cattgagtca a 51

<210> 895
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (896 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg24115035

<400> 895
agaactgttg ctttttgttt aaccacgtg caagtaaagt tcaataaagt t 51

<210> 896
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (895 is other entry)

<221> misc_feature
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<223> Accession number cg24115035

<400> 896
agaactgttg ctttttgttt aacccccgtg caagtaaagt tcaataaagt t 51

<210> 897
<211> 51
<212> DNA
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<221> misc_feature
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<400> 897
acaggccaca ccccatctc agagatggca ggcacttcac ccaaggggca g 51

<210> 898
<211> 51
<212> DNA
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<400> 898
acaggccaca ccccatctc agagaaggca ggcacttcac ccaaggggca g 51

<210> 899
<211> 51
<212> DNA
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<221> misc_feature
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<223> Accession number cg24132746

<400> 899
cctgtggtgc tgcttctcca aatgccgcc ttggtgttt cccaggagtc a 51

<210> 900
<211> 51

<212> DNA
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<223> 2 of 2 allelic variants (899 is other entry)

<221> misc_feature
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<223> Accession number cg24132746

<400> 900
cctgtggtgc tgcttctcca aatgctgccc ttggctgttt cccaggagtc a

51

<210> 901
<211> 51
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<221> misc_feature
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<223> Accession number cg24141481

<400> 901
gtgtaaagaa gtataatttc tctgccgact ccatttaatc cactgcaagg c

51

<210> 902
<211> 51
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<221> misc_feature
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<223> Accession number cg24141481

<400> 902
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51

<210> 903
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (904 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg24144955

<400> 903

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<210> 904

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (903 is other entry)

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<223> Accession number cg24144955

<400> 904

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51

<210> 905

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (906 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg25132332

<400> 905

aagtaagtgt cttaatcagg tccaagcagt aattgagaga agagagtagc t

51

<210> 906

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (905 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg25132332

<400> 906
aagtaagttg cttaatcagg tccaaacagt aattgagaga agagagtagc t 51

<210> 907
<211> 51
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<223> 1 of 2 allelic variants (908 is other entry)

<221> misc_feature
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<223> Accession number cg25132807

<400> 907
tgaactgtca ccattcttta tgtacgtgta gagatttgca gtttactgca c 51

<210> 908
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<223> 2 of 2 allelic variants (907 is other entry)

<221> misc_feature
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<223> Accession number cg25132807

<400> 908
tgaactgtca ccattcttta tgtacatgta gagatttgca gtttactgca c 51

<210> 909
<211> 51
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<222> (26)...(0)
<223> 1 of 2 allelic variants (910 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25147161

<400> 909
ctgcaatatg ccaccagcgc catggcgaac cgcactctacg ctccaattcc c 51

<210> 910
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<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (909 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

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<222> (0)...(0)

<223> Accession number cg25147161

<400> 910

ctgcaatatg ccaccagcgc catgggaacc gcatctacgc tccaattccc

50

<210> 911

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (912 is other entry)

<221> misc_feature

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<223> Accession number cg25153589

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51

<210> 912

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (911 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg25153589

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51

<210> 913

<211> 51

<212> DNA

<213> Homo sapiens

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<223> Accession number cg25153589

<400> 913
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51

<210> 914
<211> 51
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<221> misc_feature
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51

<210> 915
<211> 51
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<223> 1 of 2 allelic variants (916 is other entry)

<221> misc_feature
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ggaggatcgc ttgagcccag gagttcgaga ccagcctggg caacatagcg a

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<210> 916
<211> 51
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<221> misc_feature

<222> (0)...(0)

<223> Accession number cg25153589

<400> 916

ggaggatcgc ttgagcccag gagtttgaga ccagcctggg caacatagcg a

51

<210> 917

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (918 is other entry)

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ggccaccag ctgcctatgc tggggacggg gccgctcagg tccccaccgg g

51

<210> 918

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (917 is other entry)

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<223> Accession number cg25154211

<400> 918

ggccaccag ctgcctatgc tggggtcggg gccgctcagg tccccaccgg g

51

<210> 919

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (920 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg25154211

<400> 919

ccaccagct gcctatgctg gggacggggc cgctcaggtc cccaccgggc c

51

<210> 920
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (919 is other entry)

<221> misc_feature
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<223> Accession number cg25154211

<400> 920
ccaccagct gcctatgctg gggaccgggc cgctcaggtc cccaccgggc c 51

<210> 921
<211> 51
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<223> 1 of 2 allelic variants (922 is other entry)

<221> misc_feature
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<223> Accession number cg25154211

<400> 921
gggccgctca ggtccccacc gggcctgtgc caccggctgc ggtcctctcg c 51

<210> 922
<211> 50
<212> DNA
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<221> misc_feature
<222> (0)...(0)
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<400> 922
gggccgctca ggtccccacc gggccgtgcc accggctgag gtcctctcgc 50

<210> 923
<211> 51

<212> DNA
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<223> Accession number cg25164916

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<210> 924
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<222> (0)...(0)
<223> Accession number cg25164916

<400> 924
gataataaaa cctgccccac aatttaaaaa aaaaatcatg tcatgttagt 50

<210> 925
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<221> misc_feature
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tgtctgagct gactctaaag gaggaagaaa ggggacctag gcaaagggac c 51

<210> 926
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<223> 2 of 2 allelic variants (925 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
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<400> 926
tgtctgagct gagtctaaag gaggagaaag gggacctagg caaagggacc 50

<210> 927
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<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (928 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25167383

<400> 927
tgactgtgtg tccgggccac gtgtggctat gtgtccgggc cacgtgtgac t 51

<210> 928
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (927 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25167383

<400> 928
tgactgtgtg tccgggccac gtgtgactat gtgtccgggc cacgtgtgac t 51

<210> 929
<211> 51
<212> DNA
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<220>

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<222> (26)...(0)
<223> 1 of 2 allelic variants (930 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25171115

<400> 929
gaccacctcc ggtaccccggtgctgctgatatccgc cggcctctct g 51

<210> 930
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (929 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25171115

<400> 930
gaccacctcc ggtaccccggtgctgctgatatccgc cggcctctct g 51

<210> 931
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (932 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25171115

<400> 931
gccaaagcgtt caccacgcc tgcgtgctgc aagacctgag gaacgcgcat g 51

<210> 932
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (931 is other entry)

<221> misc_feature
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<223> Accession number cg25171115

<400> 932

gccaaagcgtt caccacgccc tgctgtctgc aagacctgag gaacgcgcat g

51

<210> 933

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (934 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg25171136

<400> 933

ttgcaggcca gtcggctggg ggaaacggat gccctgcagg gggacgggaa c

51

<210> 934

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (933 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg25171136

<400> 934

ttgcaggcca gtcggctggg ggaaatggat gccctgcagg gggacgggaa c

51

<210> 935

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (936 is other entry)

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<223> Accession number cg25171709

<400> 935

gcattgtcaa cgaaacctgc gactctcttg cttctgtgc ctgcagcatg g

51

<210> 936

<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (935 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25171709

<400> 936
gcattgtcaa cgaaacctgc gactcccttg ccttctgtgc ctgcagcatg g 51

<210> 937
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (938 is other entry)

<221> misc_feature
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<223> Accession number cg25173882

<400> 937
ttgcagtcca gctttctctc accttcaccg tggtctgtgc gcaccactga g 51

<210> 938
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (937 is other entry)

<221> misc_feature
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<223> Accession number cg25173882

<400> 938
ttgcagtcca gctttctctc acctttaccg tggtctgtgc gcaccactga g 51

<210> 939
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<220>
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<223> 1 of 2 allelic variants (940 is other entry)

<221> misc_feature
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<400> 939
atgctggaca cagggctcga caaacacaag agacgaccc t' 51

<210> 940
<211> 51
<212> DNA
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<400> 940
atgctggaca cagggctcga caaacccaag agacgaccc t 51

<210> 941
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<222> (26)...(0)
<223> 1 of 2 allelic variants (942 is other entry)

<221> misc_feature
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<223> Accession number cg25184184

<400> 941
cagtgggagc gggaagaggc cggagctcct gccccacacg tgagcaaagg g 51

<210> 942
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (941 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25184184

<400> 942
cagtggggagc ggggaagaggc cggagttcct gccccacacg tgagcaaagg g 51

<210> 943
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (944 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25237193

<400> 943
cttccaaaat gaatcccaac ttcacctgta ctagtgtttac agtccttaca c 51

<210> 944
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (943 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25237193

<400> 944
cttccaaaat gaatcccaac ttcacttgta ctagtgtttac agtccttaca c 51

<210> 945
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (946 is other entry)

<221> misc_feature
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<223> Accession number cg25239764

<400> 945
cataacctca agaagctgtg ggagcgcaac ctccaggacg atttccctca t 51

<210> 946
<211> 51

<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (945 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25239764

<400> 946
cataacctca agaagctgtg ggagcacaac ctccaggacg atttcctca t 51

<210> 947
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (948 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25244087

<400> 947
tcgtcaccac tggcgttgtc gacgttgta aaccgaggag gttcatgcgc t 51

<210> 948
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (947 is other entry)

<221> misc_feature
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<400> 948
tcgtcaccac tggcgttgtc gacgtcgta aaccgaggag gttcatgcgc t 51

<210> 949
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (950 is other entry)

<221> misc_feature
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<223> Accession number cg25244087

<400> 949
cgatcggtcc ccttcccgct ccttaagagc cttgtaggcg caccgtctgc g 51

<210> 950
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (949 is other entry)

<221> misc_feature
<222> (0)...(0)
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<400> 950
cgatcggtcc ccttcccgct ccttacgagc cttgtaggcg caccgtctgc g 51

<210> 951
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (952 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25244087

<400> 951
cgagccggac cgctcggcga gcatcggagt accaaacacg atgtcgcccg c 51

<210> 952
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (951 is other entry)

<221> misc_feature
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<400> 952
cgagccggac cgctcggcga gcatcagagt accaaacacg atgtcgcccg c 51

<210> 953
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<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (954 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25244087

<400> 953
gccggaccgc tcggcgagca tcggagtacc aaacacgatg tcgcccgcct c 51

<210> 954
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (953 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25244087

<400> 954
gccggaccgc tcggcgagca tcggaatacc aaacacgatg tcgcccgcct c 51

<210> 955
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (956 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25244087

<400> 955
ctctcttgtg aatggggacc ggacgcccg agcgaggaca gcggccgtcg a 51

<210> 956
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (955 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg25244087

<400> 956

ctctcttgtg aatggggacc ggacgtccgc agcgaggaca gcggccgtcg a

51

<210> 957

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (958 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg25248402

<400> 957

agaaaggcac agaggaaggg caaagcccca ggggagagaa aaccagtgc c

51

<210> 958

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (957 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg25248402

<400> 958

agaaaggcac agaggaaggg caaagcccag gggagagaaa accagtgcacc

50

<210> 959

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (960 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25257592

<400> 959
gaggacgaca ccgatctggc ggacgccgcc cgttcattggc gcagatacct c 51

<210> 960
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (959 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25257592

<400> 960
gaggacgaca ccgatctggc ggacgtcgcc cgttcattggc gcagatacct c 51

<210> 961
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (962 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25257592

<400> 961
ctgtcctcgg actaggcatt ttccgggtatc ttgcgtgggtg gtcattgtgc g 51

<210> 962
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (961 is other entry)

<221> misc_feature

<222> (0)...(0)
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ctgtcctcgg actaggcatt ttcggctatc ttgcgtggtg gtcattgtgc g 51

<210> 963
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (964 is other entry)

<221> misc_feature
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<223> Accession number cg25257592

<400> 963
tggtcacatc catgtcgatg gtgtgagcgt aatgaaggtc tacatcgccc t 51

<210> 964
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (963 is other entry)

<221> misc_feature
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<400> 964
tggtcacatc catgtcgatg gtgtgagcgt aatgaaggtc tacatcgccc t 51

<210> 965
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (966 is other entry)

<221> misc_feature
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<223> Accession number cg25257592

<400> 965
tcccggctgt tttcatcgtc gccggcatct ttttctggct cgccgtctaa g 51

<210> 966
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (965 is other entry)

<221> misc_feature
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<223> Accession number cg25257592

<400> 966
tcceggctgt tttcatcgtc gccggtatct tttctggct cgccgtctaa g 51

<210> 967
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (968 is other entry)

<221> misc_feature
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<223> Accession number cg25257592

<400> 967
tgtgagcgta atgaaggtct acatcgccct ggtgaaggcc tgcaccacta g 51

<210> 968
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (967 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25257592

<400> 968
tgtgagcgta atgaaggtct acatcaccct ggtgaaggcc tgcaccacta g 51

<210> 969
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (970 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25257592

<400> 969
aggtctacat cgccctggtg aaggcctgca ccactagcgt cggcaccatt t 51

<210> 970
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (969 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25257592

<400> 970
aggtctacat cgccctggtg aaggcttgca ccactagcgt cggcaccatt t 51

<210> 971
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (972 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25261577

<400> 971
tgataatagc gcttgccggt tagtggtaat acacagcttg aaatttggtg a 51

<210> 972
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (971 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg25261577

<400> 972

tgataatagc gcttgccggt tagtgataat acacagcttg aaatttggtg a

51

<210> 973

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (974 is other entry)

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<222> (0)...(0)

<223> Accession number cg25263948

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ggggcgattt caagcagaag ctcacgacga ccttcactgc gggctccggg c

51

<210> 974

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (973 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg25263948

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<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (976 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg25263948

<400> 975

cgaccttcac tgcgggctcc gggctgccc accttaccgg cgtcaagggc g

51

<210> 976

<211> 51
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<222> (26)...(0)
<223> 2 of 2 allelic variants (975 is other entry)

<221> misc_feature
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<223> Accession number cg25263948

<400> 976
cgaccttcac tgcgggctcc gggctaccgc accttaccgc cgtcaagggc g

51

<210> 977
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (978 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25263948

<400> 977
ccggtgacgc taagaagctc gtcctgtgga tgtggccaga aggcttcgac a

51

<210> 978
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (977 is other entry)

<221> misc_feature
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<223> Accession number cg25263948

<400> 978
ccggtgacgc taagaagctc gtcctatgga tgtggccaga aggcttcgac a

51

<210> 979
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (980 is other entry)

<221> misc_feature
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<223> Accession number cg25263948

<400> 979
gaaggcttcg acaagcagac gttagttgcc gtcgccaaag cgcagccgtc t 51

<210> 980
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (979 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25263948

<400> 980
gaaggcttcg acaagcagac gttagctgcc gtcgccaaag cgcagccgtc t 51

<210> 981
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (982 is other entry)

<221> misc_feature
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<223> Accession number cg25268662

<400> 981
cccttgagct ttgagctcag gtctagaggt gaacagagca gtcaccgggc g 51

<210> 982
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (981 is other entry)

<221> misc_feature
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<221> misc_feature
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<223> Accession number cg25268662

<400> 982
cccttgagct ttgagctcag gtctaaggtg aacagagcag tcaccgggcg 50

<210> 983
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (984 is other entry)

<221> misc_feature
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<223> Accession number cg25268662

<400> 983
gagctttgag ctcaggtcta gaggtgaaca gagcagtcac cgggcgactc a 51

<210> 984
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (983 is other entry)

<221> misc_feature
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<223> Accession number cg25268662

<400> 984
gagctttgag ctcaggtcta gaggtaaaca gagcagtcac cgggcgactc a 51

<210> 985
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (986 is other entry)

<221> misc_feature
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<223> Accession number cg25268662

<400> 985

agagcagtca ccgggcgact cagacgggcc agcgctcagg gtccttggt a

51

<210> 986

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (985 is other entry)

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<222> (0)...(0)

<223> Accession number cg25268662

<400> 986

agagcagtca ccgggcgact cagacgggcc agcgctcagg gtccttggt a

51

<210> 987

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (988 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg25268662

<400> 987

acgggccagc gctcagggtc cttggttaata tatgcctaga gaaaggccat g

51

<210> 988

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (987 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg25268662

<400> 988

acgggccagc gctcagggtc cttggaatat atgcctagag aaaggccatg

50

<210> 989
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (990 is other entry)

<221> misc_feature
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<223> Accession number cg25268662

<400> 989
cgggccagcg ctcagggtcc ttggtaatat atgcctagag aaaggccatg c 51

<210> 990
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (989 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25268662

<400> 990
cgggccagcg ctcagggtcc ttggtatata tgcctagaga aaggccatgc 50

<210> 991
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (992 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25310296

<400> 991
aaactccatc tcaaaaaaaaa aaaaaaatta gtttggggat accagtaatt t 51

<210> 992
<211> 50

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (991 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25310296

<400> 992
aaactccatc tcaaaaaaaaa aaaaaattag ttgggggata ccagtaattt 50

<210> 993
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (994 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25310296

<400> 993
aactccatct caaaaaaaaa aaaaaattag ttgggggata ccagtaattt c 51

<210> 994
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (993 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25310296

<400> 994
aactccatct caaaaaaaaa aaaaattagt ttgggggatac cagtaatttc 50

<210> 995
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (996 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25311248

<400> 995
cacaggcaac ccgtccagcc aagcagaagc cgtggcgtag ccgacacgcc t 51

<210> 996
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (995 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg25311248

<400> 996
cacaggcaac ccgtccagcc aagcataagc cgtggcgtag ccgacacgcc t 51

<210> 997
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (998 is other entry)

<221> misc_feature
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<223> Accession number cg25311248

<400> 997
gtccagccaa gcagaagccg tggcgtagcc gacacgcctt cgacccaacc c 51

<210> 998
<211> 51
<212> DNA
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<220>

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<222> (26)...(0)
<223> 2 of 2 allelic variants (997 is other entry)

<221> misc_feature
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<223> Accession number cg25311248

<400> 998
gtccagccaa gcagaagccg tggcgcagcc gacacgcctt cgacccaacc c

51

<210> 999
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1000 is other entry)

<221> misc_feature
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<223> Accession number cg25311248

<400> 999
tcgtgttggt cttcctcacc ctcatcccat tgacgggtcat tggttggggc a

51

<210> 1000
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (999 is other entry)

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<223> Accession number cg25311248

<400> 1000
tcgtgttggt cttcctcacc ctcatcccat tgacgggtcat tggttggggc a

51

<210> 1001
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1002 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg25311248

<400> 1001
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<210> 1002
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<223> 2 of 2 allelic variants (1001 is other entry)

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<400> 1002
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<210> 1003
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (1004 is other entry)

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<400> 1003
ccctcattcc attgacggtc attggttggg ccaacaacaa ggacctccga t 51

<210> 1004
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1003 is other entry)

<221> misc_feature
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<400> 1004
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<210> 1005

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<223> 1 of 2 allelic variants (1006 is other entry)

<221> misc_feature
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<223> Accession number cg25314764

<400> 1005
tatggaagaa aagtcactcg gaagtaccgt aaatcacccc agcgctcat c 51

<210> 1006
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1005 is other entry)

<221> misc_feature
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<223> Accession number cg25314764

<400> 1006
tatggaagaa aagtcactcg gaagtgcctg aaatcacccc agcgctcat c 51

<210> 1007
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (1008 is other entry)

<221> misc_feature
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<223> Accession number cg25314764

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aagtcactcg gaagtaccgt aaatcacccc agcgctcat cccccgaatc t 51

<210> 1008
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1007 is other entry)

<221> misc_feature
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<223> Accession number cg25314764

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aagtcactcg gaagtaccgt aaatcgcccc agcgctcat cccccgaatc t 51

<210> 1009
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<212> DNA
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<220>
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<223> 1 of 2 allelic variants (1010 is other entry)

<221> misc_feature
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<223> Accession number cg25314764

<400> 1009
gaagtaccgt aaatcacccc agcgctcat cccccgaatc tggtcgccat c 51

<210> 1010
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1009 is other entry)

<221> misc_feature
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<223> Accession number cg25314764

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gaagtaccgt aaatcacccc agcgctcat cccccgaatc tggtcgccat c 51

<210> 1011
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (1012 is other entry)

<221> misc_feature
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<223> Accession number cg25314764

<400> 1011
aatcacccca gcgcctcatc ccccgaaatct gttcgccatc tgctgtcgcc c 51

<210> 1012
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<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1011 is other entry)

<221> misc_feature
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<223> Accession number cg25314764

<400> 1012
aatcacccca gcgcctcatc ccccggaatct gttcgccatc tgctgtcgcc c 51

<210> 1013
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1014 is other entry)

<221> misc_feature
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<223> Accession number cg25314764

<400> 1013
tggtcgccat ctgctgtcgc cctgtcgctt aaggcatcac ccactagac t 51

<210> 1014
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1013 is other entry)

<221> misc_feature
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<223> Accession number cg25314764

<400> 1014
tggtcgccat ctgctgtcgc cctgtgctt aaggcatcac ccactagac t 51

<210> 1015
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1016 is other entry)

<221> misc_feature
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<400> 1015
gccatctgct gtcgcccctg cgcttaaggc atcacccac tagactgacc g

51

<210> 1016
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1015 is other entry)

<221> misc_feature
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<400> 1016
gccatctgct gtcgcccctg cgcttgaggc atcacccac tagactgacc g

51

<210> 1017
<211> 51
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<223> 1 of 2 allelic variants (1018 is other entry)

<221> misc_feature
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<223> Accession number cg25314764

<400> 1017
ggcgacatca cgggtgacgg ttcaaggtgg cagcccgagg gcccgccgtg a

51

<210> 1018
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (1017 is other entry)

<221> misc_feature
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<223> Accession number cg25314764

<400> 1018
ggcgacatca ccggtgacgg ttcaaagtgg cagcccagg gcccgcgtg a 51

<210> 1019
<211> 51
<212> DNA
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<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1020 is other entry)

<221> misc_feature
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<400> 1019
aggtggcagc ccgagggccc gccgtgaact tattgtgtcg tcttatggaa g 51

<210> 1020
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1019 is other entry)

<221> misc_feature
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<223> Accession number cg25314764

<400> 1020
aggtggcagc ccgagggccc gccgtcaact tattgtgtcg tcttatggaa g 51

<210> 1021
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1022 is other entry)

<221> misc_feature
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<223> Accession number cg25314764

<400> 1021
ggcagcccga gggcccgccg tgaacttatt gtgtcgtctt atggaagaaa a 51

<210> 1022
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1021 is other entry)

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<223> Accession number cg25314764

<400> 1022
ggcagcccga gggcccgccg tgaacatatt gtgtcgtctt atggaagaaa a 51

<210> 1023
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (1024 is other entry)

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<223> Accession number cg27297262

<400> 1023
cacacacaca cacacacaca cacacactca cccaagagtgt ttaaacaga a 51

<210> 1024
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27297262

<400> 1024
cacacacaca cacacacaca cacacctcac ccaagagtgt ttaaacagaa 50

<210> 1025
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1026 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27355682

<400> 1025
gagacaggct tgtacataaa aaaaaatact tagattaatt cctggccctg t 51

<210> 1026
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1025 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27355682

<400> 1026
gagacaggct tgtacataaa aaaaatactt agattaattc ctggccctgt 50

<210> 1027
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1028 is other entry)

<221> misc_feature
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<223> Accession number cg27360908

<400> 1027
gtgcggtatc cagcgtgaga agaaatgccg aaggtcacgg cgatgaccgc g 51

<210> 1028

<211> 51
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<223> 2 of 2 allelic variants (1027 is other entry)

<221> misc_feature
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<223> Accession number cg27360908

<400> 1028
gtgcggtatc cagcgtgaga agaaacgccg aaggtcacgg cgatgaccgc g

51

<210> 1029
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (1030 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27364539

<400> 1029
cgctcactgt gttgtccttc cttgggtatg tctcgatggt tcagcgatgg a

51

<210> 1030
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1029 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27364539

<400> 1030
cgctcactgt gttgtccttc cttggtatgt ctcgatgggt cagcgatgga

50

<210> 1031
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1032 is other entry)

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<222> (0)...(0)

<223> Accession number cg27369798

<400> 1031

cgacatcctg ttcacccagg gtgacatcat cagcagtaag tgttgcacag g

51

<210> 1032

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1031 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27369798

<400> 1032

cgacatcctg ttcacccagg gtgacgtcat cagcagtaag tgttgcacag g

51

<210> 1033

<211> 48

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1034 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27784915

<400> 1033

ccatagacac tcacctccga gtccgagatc ttctctcgc tgcggccg

48

<210> 1034

<211> 48

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1033 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27784915

<400> 1034
ccatagacac tcacctccga gtccgggatc ttctcctcgc tgcggccg

48

<210> 1035
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1036 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27794839

<400> 1035
ccttcactcg caaatcgct ctctcccccac ctccccaggc ccctcctggg a

51

<210> 1036
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1035 is other entry)

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<222> (0)...(0)
<223> Accession number cg27794839

<400> 1036
ccttcactcg caaatcgct ctctctccac ctccccaggc ccctcctggg a

51

<210> 1037
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1038 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27802892

<400> 1037

ttgctactgc taacatcctt taggcactgg gactatttct aatgcctggc a

51

<210> 1038

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1037 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

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<222> (0)...(0)

<223> Accession number cg27802892

<400> 1038

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50

<210> 1039

<211> 46

<212> DNA

<213> Homo sapiens

<220>

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<222> (21)...(0)

<223> 1 of 2 allelic variants (1040 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27804759

<400> 1039

acgcgtgccg aggcgctggg cggcggctgt gtaggttggt ggccca

46

<210> 1040

<211> 45

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1039 is other entry)

<221> misc_feature

<222> (20)...(21)

<223> Nucleotide deleted between bases 20 and 21

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27804759

<400> 1040
acgcgtgccg aggcgctggg ggcggctgtg tgagttggtg gccca 45

<210> 1041
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1042 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27804759

<400> 1041
ctgtgtgagt tgggtggccca gacgaacagc ttgtgcgaga ctctgggcat t 51

<210> 1042
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1041 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27804759

<400> 1042
ctgtgtgagt tgggtggccca gacgagcagc ttgtgcgaga ctctgggcat t 51

<210> 1043
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1044 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27805688

<400> 1043
ccagcaccag ttctgctggc cacgcgcctt gtcggcatgc agcacagggt c 51

<210> 1044
<211> 50

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1043 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27805688

<400> 1044
ccagcaccag ttctgctggc cagcccttg tcggcatgca gcacagggtc 50

<210> 1045
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1046 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27806958

<400> 1045
agcagtggaa gggcagcggc gcacagggcat atccacagcc ccattgaccc a 51

<210> 1046
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1045 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27806958

<400> 1046
agcagtggaa gggcagcggc gcacaagcat atccacagcc ccattgaccc a 51

<210> 1047
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1048 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27807001

<400> 1047
acaatgccgt taacactgcc gctggcacca gcacggctg aaccgtgacc a 51

<210> 1048
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1047 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27807001

<400> 1048
acaatgccgt taacactgcc gctggaccag catcggtga accgtgacca 50

<210> 1049
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1050 is other entry)

<221> misc_feature
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<223> Accession number cg27807001

<400> 1049
accgacttta gccttaacct tgagatccgc cttacctttg acatcgactt c 51

<210> 1050
<211> 51
<212> DNA
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<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1049 is other entry)

<221> misc_feature
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<223> Accession number cg27807001

<400> 1050
accgacttta gccttaacct tgagagccgc cttacctttg acatcgactt c 51

<210> 1051
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1052 is other entry)

<221> misc_feature
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<223> Accession number cg27807001

<400> 1051
cttctactgt cctcgaagtc gaagagagcc gagagttggg gacatcgggg g 51

<210> 1052
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1051 is other entry)

<221> misc_feature
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<400> 1052
cttctactgt cctcgaagtc gaagaaagcc gagagttggg gacatcgggg g 51

<210> 1053
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<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1054 is other entry)

<221> misc_feature
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<223> Accession number cg27807001

<400> 1053

ctgtcctcga agtcgaagag agccgagagt tggggacatc gggggcactg c

51

<210> 1054

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1053 is other entry)

<221> misc_feature

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<223> Accession number cg27807001

<400> 1054

ctgtcctcga agtcgaagag agccgggagt tggggacatc gggggcactg c

51

<210> 1055

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1056 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27807001

<400> 1055

gagccgagag ttggggacat cgggggcact gccaaagatgc atgaccgcca g

51

<210> 1056

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1055 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27807001

<400> 1056
gagccgagag ttggggacat cggggcactg ccaagatgca tgaccgccag 50

<210> 1057
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1058 is other entry)

<221> misc_feature
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<223> Accession number cg27807001

<400> 1057
gatgcatgac cgccagcgca cgttcccgag cgtacttggt caagttgtcc c 51

<210> 1058
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1057 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27807001

<400> 1058
gatgcatgac cgccagcgca cgttctcgag cgtacttggt caagttgtcc c 51

<210> 1059
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1060 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27807001

<400> 1059
acgttccgga gcgtacttgt tcaagttgtc ccgatctgcg cgagcggcgg c 51

<210> 1060
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1059 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27807001

<400> 1060

acgttcccga gcgtacttgt tcaagctgtc ccgatctgcg cgagcggcgg c

51

<210> 1061

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1062 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27825769

<400> 1061

ctgtatcttt aacagtaaaa gcgtaggaag cacatagccc caatgtattt a

51

<210> 1062

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1061 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27825769

<400> 1062

ctgtatcttt aacagtaaaa gcgtacgaag cacatagccc caatgtattt a

51

<210> 1063

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1064 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27826716

<400> 1063
cgttggttga gaaggatgtc accaactgag gtatcgagat ctcatgccca c 51

<210> 1064
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1063 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27826716

<400> 1064
cgttggttga gaaggatgtc accaattgag gtatcgagat ctcatgccca c 51

<210> 1065
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1066 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27831266

<400> 1065
taaggctgtg gaggagccag atgggggacta gcctctggac ttctgcttag g 51

<210> 1066
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1065 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27831266

<400> 1066

taaggctgtg gaggagccag atgggaacta gcctctggac ttctgcttag g

51

<210> 1067

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1068 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27831595

<400> 1067

gggcctcagg gtaagctgga gttgcgggcc accgcccag gagttgagt g

51

<210> 1068

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1067 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27831595

<400> 1068

gggcctcagg gtaagctgga gttgcggcca ccgcccag agttgagtgg

50

<210> 1069

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1070 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27834324

<400> 1069

catggagtca ctcagatcac gcatcgagga aagcactaag gtaacaccca g

51

<210> 1070
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1069 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27834324

<400> 1070
catggagtca ctcagatcac gcatcaagga aagcactaag gtaacaccca g

51

<210> 1071
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1072 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27835768

<400> 1071
cagctgttgt gtgcctggca gcgctgcttt cagccccatt cattccaac t

51

<210> 1072
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1071 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27835768

<400> 1072
cagctgttgt gtgcctggca gcgctctttc agccccattc attccaact

50

<210> 1073
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1074 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27837446

<400> 1073
tgtttgctat tttatttttt gagacagggtc tcattctgcc attcaggctg a 51

<210> 1074
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1073 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27837446

<400> 1074
tgtttgctat tttatttttt gagacgggtc tcattctgcc attcaggctg a 51

<210> 1075
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1076 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27837446

<400> 1075
tgtacgtgtg tgtgtgtgtg tgtgtgtaag tgtctgtgtg tacgtgtaag t 51

<210> 1076
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1075 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

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<223> Accession number cg27837446

<400> 1076

tgtacgtgtg tgtgtgtgtg tgtgttaagt gtctgtgtgt acgtgtaagt

50

<210> 1077

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1078 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27838870

<400> 1077

cgacaactcg atcgaccga ggcgcgacac ccgcctgccc cgtactttcc c

51

<210> 1078

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1077 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27838870

<400> 1078

cgacaactcg atcgaccga ggcgcaacac ccgcctgccc cgtactttcc c

51

<210> 1079

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1080 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27838870

<400> 1079
actttccgc catcccaagt caccggtgtg tcgctcgta gcatcgctc a 51

<210> 1080
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1079 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27838870

<400> 1080
actttccgc catcccaagt caccggtgtg tcgctcgta gcatcgctc a 51

<210> 1081
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1082 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27840665

<400> 1081
tgataggaag gatgcgcaga ttgttgtct taccggaat atccatcggg g 51

<210> 1082
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1081 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27840665

<400> 1082
tgataggaag gatgcgcaga ttgttgtct taccggaat atccatcggg g 51

<210> 1083
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1084 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27840665

<400> 1083
gcagattggt ggtcttacct ggaatatcca tcggggaacc ggacaacacg a

51

<210> 1084
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1083 is other entry)

<221> misc_feature
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<223> Accession number cg27840665

<400> 1084
gcagattggt ggtcttacct ggaatgtcca tcggggaacc ggacaacacg a

51

<210> 1085
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1086 is other entry)

<221> misc_feature
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<223> Accession number cg27840665

<400> 1085
gacaacacga cgacgcggtc accgaccggc acgaaaccct tgtcgcgcag g

51

<210> 1086
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1085 is other entry)

<221> misc_feature
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<223> Accession number cg27840665

<400> 1086
gacaacacga cgacgcggtc accgatcggc acgaaaccct tgcgcgcag g 51

<210> 1087
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1088 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27842663

<400> 1087
ctagcctgga gtcaggagac agcaagagta ggggctgagg ttgtggggcc 50

<210> 1088
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1087 is other entry)

<221> misc_feature
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<223> Accession number cg27842663

<400> 1088
ctagcctgga gtcaggagac agcaaagagt aggggctgag gttgtggggc c 51

<210> 1089
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1090 is other entry)

<221> misc_feature
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<221> misc_feature
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<223> Accession number cg27842663

<400> 1089
ctagcctgga gtcaggagac agcaagagta ggggctgagg ttgtggggcc 50

<210> 1090
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> Accession number cg27842663

<400> 1090
ctagcctgga gtcaggagac agcaaagagt aggggctgag gttgtggggc c 51

<210> 1091
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1092 is other entry)

<221> misc_feature
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<223> Accession number cg27842663

<400> 1091
gagacagcaa gtagtaggggc tgaggttgtg gggcccaggg tcccagtgtg g 51

<210> 1092
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1091 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27842663

<400> 1092
gagacagcaa gagtaggggc tgagggtgtg gggcccaggg tcccagtga g 51

<210> 1093
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1094 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27843594

<400> 1093
aggtacagct caggaaggc agcagccct tgctcaggt ctttctggc a 51

<210> 1094
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1093 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27843594

<400> 1094
aggtacagct caggaaggc agcagccct gctcaggtc ctttctggc a 50

<210> 1095
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1096 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27843890

<400> 1095

cgtaggttgac gatctcgccg gtggaggcgt ccttgacgac gatctggcca c

51

<210> 1096

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1095 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27843890

<400> 1096

cgtaggttgac gatctcgccg gtggaagcgt ccttgacgac gatctggcca c

51

<210> 1097

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1098 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27843890

<400> 1097

tggacttcgt cggctctgcgg tacgacgaag ggctcaacat tgccggtggc a

51

<210> 1098

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1097 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27843890

<400> 1098

tggacttcgt cggctctgcgg tacgatgaag ggctcaacat tgccggtggc a

51

<210> 1099
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1100 is other entry)

<221> misc_feature
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<223> Accession number cg27843890

<400> 1099
acgaagggt caacattgcc ggtggcatcg atgatgagtt tgctgcctg g 51

<210> 1100
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1099 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27843890

<400> 1100
acgaagggt caacattgcc ggtggatcga tgatgagttt gctgcctgg 50

<210> 1101
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1102 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27843890

<400> 1101
tgagtttgct cgctgggca acacctagca gcaatggcat cgatagtcct t 51

<210> 1102
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1101 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27843890

<400> 1102
tgagtttgct cgcctgggca acaccagca gcaatggcat cgatagtcct t 51

<210> 1103
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1104 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27844015

<400> 1103
ggtaatgcgg aacgcacgtg cctgcgttca gactccattt atcttcaccg t 51

<210> 1104
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1103 is other entry)

<221> misc_feature
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<223> Accession number cg27844015

<400> 1104
ggtaatgcgg aacgcacgtg cctgcattca gactccattt atcttcaccg t 51

<210> 1105
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 1 of 2 allelic variants (1106 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27845127

<400> 1105
gagcgtgcgc catgatgccg cgactgacac cacctgcggt ccagcccaaa a 51

<210> 1106
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1105 is other entry)

<221> misc_feature
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<223> Accession number cg27845127

<400> 1106
gagcgtgcgc catgatgccg cgactcacac cacctgcggt ccagcccaaa a 51

<210> 1107
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1108 is other entry)

<221> misc_feature
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<223> Accession number cg27845127

<400> 1107
aaaatcgggt gcttcttcat accaatcacg aggaggtcaa cgttgccca g 51

<210> 1108
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1107 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27845127

<400> 1108
aaaatcgggt gcttcttcat accaaccacg aggaggtcaa cgttgcccga g 51

<210> 1109
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1110 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27845127

<400> 1109
cataccaatc acgaggaggt caacggtgcc cgagaggtcg actaaggcgt c 51

<210> 1110
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1109 is other entry)

<221> misc_feature
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<223> Accession number cg27845127

<400> 1110
cataccaatc acgaggaggt caacgctgcc cgagaggtcg actaaggcgt c 51

<210> 1111
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1112 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27845127

<400> 1111
caacggtgcc cgagaggtcg actaaggcgt cgacgggttc tccggacagc a 51

<210> 1112
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1111 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27845127

<400> 1112

caacgttgcc cgagaggtcg actaaagcgt cgacgggttc tccggacagc a

51

<210> 1113

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1114 is other entry)

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<222> (0)...(0)

<223> Accession number cg27845127

<400> 1113

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51

<210> 1114

<211> 51

<212> DNA

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1113 is other entry)

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<223> Accession number cg27845127

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agaggtcgac taaggcgctcg acgggtcttc cggacagcac gcgggtctcg a

51

<210> 1115

<211> 47

<212> DNA

<213> Homo sapiens

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<222> (22)...(0)

<223> 1 of 2 allelic variants (1116 is other entry)

<221> misc_feature
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<223> Accession number cg27845127

<400> 1115
acgcgtcctg aagccgccga cgcgacgaga acagcaggcc agcagct

47

<210> 1116
<211> 47
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1115 is other entry)

<221> misc_feature
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<223> Accession number cg27845127

<400> 1116
acgcgtcctg aagccgccga cgcgacgaga acagcaggcc agcagct

47

<210> 1117
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (1118 is other entry)

<221> misc_feature
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<223> Accession number cg27845127

<400> 1117
gttctccgga cagcacgcgg gtctcgacct cgacatgggg atgcttatta g

51

<210> 1118
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1117 is other entry)

<221> misc_feature
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gttctccgga cagcacgcgg gtctctacct cgacatgggg atgcttatta g

51

<210> 1119

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1120 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27845127

<400> 1119

gtctcgacct cgacatgggg atgcttatta gcgagcggct tgacgacctc g

51

<210> 1120

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1119 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27845127

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gtctcgacct cgacatgggg atgctcatta gcgagcggct tgacgacctc g

51

<210> 1121

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1122 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27845127

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51

<210> 1122

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1121 is other entry)

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<223> Accession number cg27845127

<400> 1122
cgacctcgac atggggatgc ttattggcga gcggcttgac gacctcgttg a 51

<210> 1123
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (1124 is other entry)

<221> misc_feature
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<223> Accession number cg27845127

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<210> 1124
<211> 51
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<220>
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<223> 2 of 2 allelic variants (1123 is other entry)

<221> misc_feature
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<223> Accession number cg27845127

<400> 1124
gatgcttatt agcgagcggc ttgacaacct cgttgagtcg tttgagggcc t 51

<210> 1125
<211> 48
<212> DNA
<213> Homo sapiens

<220>
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<222> (24)...(0)
<223> 1 of 2 allelic variants (1126 is other entry)

<221> misc_feature
<222> (23)...(24)
<223> Nucleotide deleted between bases 23 and 24

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27845621

<400> 1125
ggatcctgtg ccagccgagg aggtccttcc caggctctct caagggtc

48

<210> 1126
<211> 49
<212> DNA
<213> Homo sapiens

<220>
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<222> (24)...(0)
<223> 2 of 2 allelic variants (1125 is other entry)

<221> misc_feature
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<223> Accession number cg27845621

<400> 1126
ggatcctgtg ccagccgagg aggtccttcc ccaggctctc tcaagggtc

49

<210> 1127
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1128 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27845788

<400> 1127
gcgttttggt aatgagcctg agcagtcatt ctggaccgcc caggctccca g

51

<210> 1128
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1127 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg27845788

<400> 1128

gcgttttgggt aatgagcctg agcagccatg ctggaccgcc caggctccca g

51

<210> 1129

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> 1 of 2 allelic variants (1130 is other entry)

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<222> (0)...(0)

<223> Accession number cg27846188

<400> 1129

ttcaaatacca gttcttccac agcaaccagc ccatagttgt tctgtgttct t

51

<210> 1130

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1129 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27846188

<400> 1130

ttcaaatacca gttcttccac agcaatcagc ccatagttgt tctgtgttct t

51

<210> 1131

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1132 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27846188

<400> 1131

ttccacagca accagcccat agttgttctg tgttcttcca cagctgttta c

51

<210> 1132

<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1131 is other entry)

<221> misc_feature
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<223> Accession number cg27846188

<400> 1132
ttccacagca accagcccat agttgctctg tgttcttcca cagctgttta c 51

<210> 1133
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1134 is other entry)

<221> misc_feature
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<223> Accession number cg27846188

<400> 1133
tgttcttcca cagctgttta cggtagcctc ctagccactc tcttcagcaa g 51

<210> 1134
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1133 is other entry)

<221> misc_feature
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<223> Accession number cg27846188

<400> 1134
tgttcttcca cagctgttta cggtaacctc ctagccactc tcttcagcaa g 51

<210> 1135
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1136 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27846188

<400> 1135
tacctcactt cctccaccgc tcttcagccc ctttgatgtc ccctcagaga a 51

<210> 1136
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1135 is other entry)

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<223> Accession number cg27846188

<400> 1136
tacctcactt cctccaccgc tcttcgcccc ctttgatgtc ccctcagaga a 51

<210> 1137
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1138 is other entry)

<221> misc_feature
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<223> Accession number cg27846188

<400> 1137
actagatcca ctgtgctttc cttcaaattc agttcttcca cagcaaccag c 51

<210> 1138
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1137 is other entry)

<221> misc_feature
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<223> Accession number cg27846188

<400> 1138
actagatcca ctgtgctttc cttcagatcc agttcttcca cagcaaccag c 51

<210> 1139
<211> 46
<212> DNA
<213> Homo sapiens

<220>
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<222> (21)...(0)
<223> 1 of 2 allelic variants (1140 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27847752

<400> 1139
gcgcgccctc cctgggtgac aggctgtact tctttcacaa aaggac 46

<210> 1140
<211> 46
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (21)...(0)
<223> 2 of 2 allelic variants (1139 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27847752

<400> 1140
gcgcgccctc cctgggtgac gggctgtact tctttcacaa aaggac 46

<210> 1141
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1142 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27847752

<400> 1141
tgaggccatt cttgcactgc tataaagaaa tacccgagac tgggtaattt a 51

<210> 1142
<211> 51

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1141 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27847752

<400> 1142
tgaggccatt cttgcactgc tataacgaaa taccgagac tgggtaattt a 51

<210> 1143
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1144 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27850121

<400> 1143
cgtcgccgaa aagccaggcc cggaggtgcc taagtcaggg accgagacgc a 51

<210> 1144
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1143 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27850121

<400> 1144
cgtcgccgaa aagccaggcc cggagtgccct aagtcagggc cagagacgca 50

<210> 1145
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1146 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27922967

<400> 1145
cgcggtgttac caggaaggg gacaggattc ttgcacttt taccctttc t 51

<210> 1146
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1145 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27922967

<400> 1146
cgcggtgttac caggaaggg gacagaattc ttgcacttt taccctttc t 51

<210> 1147
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1148 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27926321

<400> 1147
catcacctcc ctgactgcct ctctaccac ctcccatcac ctccctgact g 51

<210> 1148
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1147 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27926321

<400> 1148
catcacctcc ctgactgcct ctctctccac ctcccatcac ctccctgact g 51

<210> 1149
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1150 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27926378

<400> 1149
atgggatgtt ctgtttttgt ctgtaaagg aaagggatca tttatgttca a 51

<210> 1150
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1149 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27926378

<400> 1150
atgggatgtt ctgtttttgt ctgtagagg aaagggatca tttatgttca a 51

<210> 1151
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1152 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27926378

<400> 1151
ttaggaagt aattaagagg ctgtgcctc tgtcacatcc aagtttctgc c 51

<210> 1152
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1151 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27926378

<400> 1152
ttagggaagt aattaagagg ctgtgcctct gtcacatcca agtttctgcc

50

<210> 1153
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1154 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27926378

<400> 1153
aggaagtaa ttaagaggct gtgccctctg tcacatccaa gtttctgccc a

51

<210> 1154
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1153 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27926378

<400> 1154
agggaagtaa ttaagaggct gtgcctctgt cacatccaag tttctgccca 50

<210> 1155
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1156 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27926927

<400> 1155
atcttaagac cctcgatgga tgttgatgcg ggccgcccgg tcggcgaagg g 51

<210> 1156
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1155 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27926927

<400> 1156
atcttaagac cctcgatgga tgttgatgcg ggccgcccgg tcggcgaagg g 51

<210> 1157
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1158 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27928117

<400> 1157
gtggtggagg tcggggcatg ggggtcccca gccatgttca gattcctgta g 51

<210> 1158
<211> 50
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1157 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27928117

<400> 1158

gtggtggagg tcggggcatg ggggtgccag ccattgttcag attcctgtag

50

<210> 1159

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1160 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27928408

<400> 1159

accttgggga gggcgggtag aggccgagga atctgcaggc gcagaggaca g

51

<210> 1160

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1159 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27928408

<400> 1160

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51

<210> 1161

<211> 51

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1162 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27930889

<400> 1161
acaattagat gtagtggttag tctgacgatg tgataagaaa acctccccag c 51

<210> 1162
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1161 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27930889

<400> 1162
acaattagat gtagtggttag tctgatgatg tgataagaaa acctccccag c 51

<210> 1163
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1164 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27931448

<400> 1163
aaccaccacc ttcggccgcc ccgcgcgcca gccagcccggt acgcgctcac c 51

<210> 1164
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1163 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg27931448

<400> 1164
aaccaccacc ttcggccgcc ccgcgagcca gccagcccg acgcgctcac c 51

<210> 1165
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1166 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27931448

<400> 1165
agccagcccg tacgcgctca cccacaggaa cccctcgtc cagtcctca c 51

<210> 1166
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1165 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27931448

<400> 1166
agccagcccg tacgcgctca cccacgggaa cccctcgtc cagtcctca c 51

<210> 1167
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1168 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27931448

<400> 1167
ccgtacgcgc tcaccacag gaacccctc gtccagtc tcaactaccc t 51

<210> 1168
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1167 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27931448

<400> 1168
ccgtacgcgc tcacccacag gaacctcctc gtccagtcctc tcaactacccc t 51

<210> 1169
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1170 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27931448

<400> 1169
gcgctcaccc acaggaaccc cctcgtccag tccctcacta cccctcaggc c 51

<210> 1170
<211> 51
<212> DNA
<213> Homo sapiens

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<400> 1170
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<210> 1171
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<223> 1 of 2 allelic variants (1172 is other entry)

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<223> Accession number cg27931448

<400> 1171
acccacagga accccctcgt ccagtccttc actacccttc aggccctgta a 51

<210> 1172
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (1171 is other entry)

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<223> Accession number cg27931448

<400> 1172
acccacagga accccctcgt ccagtccttc actacccttc aggccctgta a 51

<210> 1173
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (1174 is other entry)

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<400> 1173
ccacaggaac cccctcgtcc agtcctcac taccctcag gccctgtcaa g 51

<210> 1174
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (1173 is other entry)

<221> misc_feature
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<223> Accession number cg27931448

<400> 1174

ccacaggaac cccctcgtec agtccttcac taccctcag gccctgtcaa g

51

<210> 1175

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1176 is other entry)

<221> misc_feature

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<223> Accession number cg27931448

<400> 1175

cgtccagtc ctcactaccc ctcaggccct gtcaagccgg cgccggcgca g

51

<210> 1176

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1175 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27931448

<400> 1176

cgtccagtc ctcactaccc ctcagaccct gtcaagccgg cgccggcgca g

51

<210> 1177

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1178 is other entry)

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<222> (0)...(0)

<223> Accession number cg27933823

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cgttaacctc ccacctctgc aatcttgccc gacacctaga tacctgctg c

51

<210> 1178

<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1177 is other entry)

<221> misc_feature
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<223> Accession number cg27933823

<400> 1178
cgттаacctc ccacctctgc aatctagccc gacacctaga tacctgcgtg c

51

<210> 1179
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1180 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27955069

<400> 1179
aaaaaaagaa aaaagaaaaa aaaaaagaat gcagtctgtc catttttgtg c

51

<210> 1180
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1179 is other entry)

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<223> Accession number cg27955069

<400> 1180
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50

<210> 1181
<211> 51
<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1182 is other entry)

<221> misc_feature
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<223> Accession number cg27957329

<400> 1181
gccgcgggct gagattttcg tctgcccc ctcctgccg ccagcgctt a 51

<210> 1182
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1181 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg27957329

<400> 1182
gccgcgggct gagattttcg tctgcccc tccctgccg ccagcgcta 50

<210> 1183
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1184 is other entry)

<221> misc_feature
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<223> Accession number cg27958374

<400> 1183
gattggctgt acaggatagc gaatgctgtg gttggagggc acagtcttcc c 51

<210> 1184
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1183 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg27958374

<400> 1184
gattggctgt acaggatagc gaatgtgtgg ttggagggca cagtcttccc 50

<210> 1185
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (1186 is other entry)

<221> misc_feature
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<223> Accession number cg27958800

<400> 1185
agtggcagga gagaggagat gggggcgtgg cagtgagcga tgaggtcaat c 51

<210> 1186
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1185 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27958800

<400> 1186
agtggcagga gagaggagat gggggtgtgg cagtgagcga tgaggtcaat c 51

<210> 1187
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1188 is other entry)

<221> misc_feature
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<223> Accession number cg27958800

<400> 1187
gagatggggg cgtggcagtg agcgatgagg tcaatctgac gaggcctgtg g 51

<210> 1188
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1187 is other entry)

<221> misc_feature
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<223> Accession number cg27958800

<400> 1188
gagatggggg cgtggcagtg agcgacgagg tcaatctgac gaggcctgtg g 51

<210> 1189
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1190 is other entry)

<221> misc_feature
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<223> Accession number cg27958800

<400> 1189
tttggcttca gctaaggag atggccgcca ctgtggagtt ttggggcaga g 51

<210> 1190
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<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (1189 is other entry)

<221> misc_feature
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<223> Accession number cg27958800

<400> 1190
tttggcttca gctaaggag atggcagcca ctgtggagtt ttggggcaga g 51

<210> 1191
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1192 is other entry)

<221> misc_feature
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<223> Accession number cg27958800

<400> 1191
ccgccactgt ggagtttttg ggagagggga catgctctga cttcccttta a 51

<210> 1192
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1191 is other entry)

<221> misc_feature
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<223> Accession number cg27958800

<400> 1192
ccgccactgt ggagtttttg ggagagggga catgctctga cttcccttta a 51

<210> 1193
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<212> DNA
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<223> 1 of 2 allelic variants (1194 is other entry)

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<223> Accession number cg27958800

<400> 1193
tctgacttcc ctttaaattg gtcacatgg ctctacgct gagggactac a 51

<210> 1194
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<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1193 is other entry)

<221> misc_feature
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<223> Accession number cg27958800

<400> 1194
tctgacttcc ctttaaattgg gtcgatgatgg ctctacgct gagggactac a

51

<210> 1195
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1196 is other entry)

<221> misc_feature
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catggctcct acgctgaggg actacagggg agaaggggag aaagaccagt t

51

<210> 1196
<211> 50
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<400> 1196
catggctcct acgctgaggg actacgggga gaaggggaga aagaccagtt

50

<210> 1197
<211> 51
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<223> 1 of 2 allelic variants (1198 is other entry)

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<223> Accession number cg27958800

<400> 1197
cttgagcgcg ccagggacag tggagaccag agtggcagga gagaggagat g 51

<210> 1198
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (1197 is other entry)

<221> misc_feature
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<400> 1198
cttgagcgcg ccagggacag tggaggccag agtggcagga gagaggagat g 51

<210> 1199
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1200 is other entry)

<221> misc_feature
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<223> Accession number cg27961578

<400> 1199
tatggaagag agagagagag agagagtttt tttttcacat ctgaattgat g 51

<210> 1200
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1199 is other entry)

<221> misc_feature
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<400> 1200
tatggaagag agagagagag agagattttt ttttcacatc tgaattgatg 50

<210> 1201
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1202 is other entry)

<221> misc_feature
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<223> Accession number cg27962034

<400> 1201
gcccgcccga ccaagcgtcg gacgcggccc ggcgccgagc catggagcct g 51

<210> 1202
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1201 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg27962034

<400> 1202
gcccgcccga ccaagcgtcg gacgcgcccg gcgccgagcc atggagcctg 50

<210> 1203
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1204 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg27963505

<400> 1203

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51

<210> 1204

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1203 is other entry)

<221> misc_feature

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<223> Accession number cg27963505

<400> 1204

cccttcgagg cccggaaga cctccgacc cgctgacaat gctgggcct c

51

<210> 1205

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1206 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28098037

<400> 1205

gaatggagat aaaagggaat aacaattcaa ctagaaggag aagaagtcct g

51

<210> 1206

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1205 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28098037

<400> 1206
gaatggagat aaaaggaat aacaactcaa ctagaaggag aagaagtcct g 51

<210> 1207
<211> 51
<212> DNA
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<221> misc_feature
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<223> 1 of 2 allelic variants (1208 is other entry)

<221> misc_feature
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<223> Accession number cg28104192

<400> 1207
taactaccga gagtgggtat ttatctagag agatagaggc ttttggagca g 51

<210> 1208
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (1207 is other entry)

<221> misc_feature
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<223> Accession number cg28104192.

<400> 1208
taactaccga gagtgggtat ttatcaagag agatagaggc ttttggagca g 51

<210> 1209
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1210 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28117507

<400> 1209
aggcggaagc tgctccggtg ttgttggtc agtgtgccga tgccggcgtc a 51

<210> 1210
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1209 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28117507

<400> 1210

aggcgggaagc tgctccggtg ttgttagctc agtgtgccga tgccggcgtc a

51

<210> 1211

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1212 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28117507

<400> 1211

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51

<210> 1212

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1211 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28117507

<400> 1212

agtgtgccga tgccggcgtc aagcctttgt tggagggtcc agactggggt t

51

<210> 1213

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1214 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28117507

<400> 1213
ccggcggtcaa gcctttgttg gaggggtccag actgggggttt attggatcga c

51

<210> 1214
<211> 51
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<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1213 is other entry)

<221> misc_feature
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<223> Accession number cg28117507

<400> 1214
ccggcggtcaa gcctttgttg gaggggtccag actgggggttt attggatcga c

51

<210> 1215
<211> 51
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1216 is other entry)

<221> misc_feature
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<223> Accession number cg28350841

<400> 1215
gggacttgga caggcacggg ccctggcatg gcggggccagg tccacctcgg c

51

<210> 1216
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<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1215 is other entry)

<221> misc_feature
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<222> (0)...(0)
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<400> 1216
gggacttgga caggcacggg ccctgcatgg cgggccaggt ccacctcggc 50

<210> 1217
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<212> DNA
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<220>
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<223> 1 of 2 allelic variants (1218 is other entry)

<221> misc_feature
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<223> Accession number cg28375854

<400> 1217
gcggggggccc agccatcttg cacttaatgg atggcacacg aggccagctg c 51

<210> 1218
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1217 is other entry)

<221> misc_feature
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<223> Accession number cg28375854

<400> 1218
gcggggggccc agccatcttg cacttgatgg atggcacacg aggccagctg c 51

<210> 1219
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (1220 is other entry)

<221> misc_feature
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<223> Accession number cg28376296

<400> 1219
aacggagtaa gcgataaaga gtccgtagat gaacaccgcg ccgctgagga t 51

<210> 1220
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<212> DNA
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<220>
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<223> 2 of 2 allelic variants (1219 is other entry)

<221> misc_feature
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<223> Accession number cg28376296

<400> 1220
aacggagtaa gcgataaaga gtccgagatg aacaccgcgc cgctgaggat

50

<210> 1221
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<223> 1 of 2 allelic variants (1222 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28388611

<400> 1221
agatagatag atagatagat agatgataga tagatagata gatagataga t

51

<210> 1222
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1221 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg28388611

<400> 1222

agatagatag atagatagat agatgtagat agatagatag atagatagat

50

<210> 1223

<211> 51

<212> DNA

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<223> Accession number cg28388611

<400> 1223

atagatagat agatagatag atgatagata gatagataga tagatagata g

51

<210> 1224

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1223 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28388611

<400> 1224

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50

<210> 1225

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1226 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28389525

<400> 1225

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51

<210> 1226

<211> 51

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<223> Accession number cg28389525

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51

<210> 1227

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (1228 is other entry)

<221> misc_feature

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<223> Accession number cg28389525

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51

<210> 1228

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1227 is other entry)

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<223> Accession number cg28389525

<400> 1228

tcacgaagcg tttgggagtg gatgcagaaa gtgtacataa aaccaatccg c

51

<210> 1229

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1230 is other entry)

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ttcgggtcaag aggggccgtt ccgaaatcgt cccgcgtatg atctcattgt a 51

<210> 1230
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<400> 1230
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<210> 1231
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<223> 1 of 2 allelic variants (1232 is other entry)

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<223> Accession number cg28389525

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<210> 1232
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<213> Homo sapiens

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<223> 2 of 2 allelic variants (1231 is other entry)

<221> misc_feature
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<223> Accession number cg28389525

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taaatttcaa agatcccaag gaccacgagc gtttcatgaa gctcgttgag c

51

<210> 1233

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1234 is other entry)

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<223> Accession number cg28389807

<400> 1233

accttctgta tgctggcatt gcagaccag caaggagcca aacgaatgaa a

51

<210> 1234

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1233 is other entry)

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<223> Accession number cg28389807

<400> 1234

accttctgta tgctggcatt gcagatccag caaggagcca aacgaatgaa a

51

<210> 1235

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1236 is other entry)

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<223> Accession number cg28396311

<400> 1235

gcacgaggcc tgacactttg cgggagccct ggaggaaaca ggtggttgc g

51

<210> 1236

<211> 50
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<221> misc_feature
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<400> 1236
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50

<210> 1237
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<223> 1 of 2 allelic variants (1238 is other entry)

<221> misc_feature
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<400> 1237
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51

<210> 1238
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<212> DNA
<213> Homo sapiens

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<223> Accession number cg28397512

<400> 1238
ttttgctgtc agcaaccata gccacaggta taccagcttc tgcattttct g

51

<210> 1239
<211> 51
<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (1240 is other entry)

<221> misc_feature

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<223> Accession number cg28397512

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51

<210> 1240

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

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<223> Accession number cg28397512

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gcctccacct gtgctagggtg ggccctctgg gttctaaggc atctctgtat

50

<210> 1241

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1242 is other entry)

<221> misc_feature

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<223> Accession number cg28399769

<400> 1241

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51

<210> 1242

<211> 50

<212> DNA

<213> Homo sapiens

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<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28399769

<400> 1242
gggtccaggg aggagagcgc ggcgcggcgg ctgagcgcga agagggagtg 50

<210> 1243
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1244 is other entry)

<221> misc_feature
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<223> Accession number cg28453626

<400> 1243
gagtggttca ccttttactt ggtcaatcag ggggtttgtg ttcccaggaa c 51

<210> 1244
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (1243 is other entry)

<221> misc_feature
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<223> Accession number cg28453626

<400> 1244
gagtggttca ccttttactt ggtcagtcag ggggtttgtg ttcccaggaa c 51

<210> 1245
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1246 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28458642

<400> 1245
ggaaggctcag acccgcgtca cccgcgaacg aaatggcctc ggatgcgtca g 51

<210> 1246
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1245 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28458642

<400> 1246
ggaaggctcag acccgcgtca cccgcaaacg aaatggcctc ggatgcgtca g 51

<210> 1247
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1248 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28464065

<400> 1247
tgtccacgaa atacacccca aaccggaagc cttctctcca ccaagtccaa g 51

<210> 1248
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1247 is other entry)

<221> misc_feature
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<223> Accession number cg28464065

<400> 1248
tgtccacgaa atacaccca aacccaaagc cttctctcca ccaagtccaa g 51

<210> 1249
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1250 is other entry)

<221> misc_feature
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<223> Accession number cg28464080

<400> 1249
gtggatggca gccagagaga ctgctgaggt tctggatggt agggccttga t 51

<210> 1250
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1249 is other entry)

<221> misc_feature
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<223> Accession number cg28464080

<400> 1250
gtggatggca gccagagaga ctgctcaggt tctggatggt agggccttga t 51

<210> 1251
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1252 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28464080

<400> 1251
ggggacagcc gagggcgagt ggtcttggaa gcgtgccatg tgcaggacac a 51

<210> 1252
<211> 51

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1251 is other entry)

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<223> Accession number cg28464080

<400> 1252
ggggacagcc gagggcgagt ggtctcggaa gcgtgccatg tgcaggacac a

51

<210> 1253
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (1254 is other entry)

<221> misc_feature
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<223> Accession number cg28473092

<400> 1253
tggcgagggt cagcagtctt ctcggcgctcg tcaggctcgag catggtactc g

51

<210> 1254
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1253 is other entry)

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<400> 1254
tggcgagggt cagcagtctt ctcgggtgctg tcaggctcgag catggtactc g

51

<210> 1255
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1256 is other entry)

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<222> (0)...(0)

<223> Accession number cg28473092

<400> 1255

gacgggtaag gatttgcgag ctaataacga tcggagcgctc accctcgagc a

51

<210> 1256

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1255 is other entry)

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<223> Accession number cg28473092

<400> 1256

gacgggtaag gatttgcgag ctaatgacga tcggagcgctc accctcgagc a

51

<210> 1257

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1258 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28473092

<400> 1257

ggatttgcga gctaataacg atcggagcgt caccctcgag catcgtcacc t

51

<210> 1258

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (1257 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28473092

<400> 1258
ggatttgca gctaataacg atcggggcgt caccctcgag catcgtcacc t 51

<210> 1259
<211> 51
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<223> 1 of 2 allelic variants (1260 is other entry)

<221> misc_feature
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<223> Accession number cg28473092

<400> 1259
gcgagctaata aacgatcgga gcgtcaccct cgagcatcgt cacctcgatg c 51

<210> 1260
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1259 is other entry)

<221> misc_feature
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<223> Accession number cg28473092

<400> 1260
gcgagctaata aacgatcgga gcgtcgccct cgagcatcgt cacctcgatg c 51

<210> 1261
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1262 is other entry)

<221> misc_feature
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<223> Accession number cg28473092

<400> 1261
cgatgctaata tagagccatg tgccgatgag tgaaggagac catccgcgag g 51

<210> 1262
<211> 51
<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1261 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28473092

<400> 1262

cgatgctaata tagagccatg tgccggtgag tgaaggagac catccgag g

51

<210> 1263

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (1264 is other entry)

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<222> (0)...(0)

<223> Accession number cg28473092

<400> 1263

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51

<210> 1264

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1263 is other entry)

<221> misc_feature

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<223> Accession number cg28473092

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51

<210> 1265

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1266 is other entry)

<221> misc_feature
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<223> Accession number cg28473092

<400> 1265
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<210> 1266
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (1265 is other entry)

<221> misc_feature
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<223> Accession number cg28473092

<400> 1266
gtttatacga ctggatctcg ttgatgctga gcaggagtgg ttcgtcatcc a 51

<210> 1267
<211> 47
<212> DNA
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<220>
<221> misc_feature
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<223> 1 of 2 allelic variants (1268 is other entry)

<221> misc_feature
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<223> Accession number cg28473115

<400> 1267
tcatgaaatg tttgttgga aggtaccatt taaccttttt ttccaat 47

<210> 1268
<211> 47
<212> DNA
<213> Homo sapiens

<220>
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<222> (22)...(0)
<223> 2 of 2 allelic variants (1267 is other entry)

<221> misc_feature
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<223> Accession number cg28473115

<400> 1268

tcatgaaatg tttgttggtgta aagtaccatt taaccttttt ttccaat

47

<210> 1269

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1270 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28785423

<400> 1269

gggttttagct agcatgtagc aagcccttaa tgactgcagc tattatcata a

51

<210> 1270

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1269 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28785423

<400> 1270

gggttttagct agcatgtagc aagcccttaa tgactgcagc tattatcata a

51

<210> 1271

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1272 is other entry)

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<222> (0)...(0)

<223> Accession number cg28785423

<400> 1271

atgtagcaag cccttaatga ctgcagctat tatkataatt agctctgtat g

51

<210> 1272

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1271 is other entry)

<221> misc_feature
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<223> Accession number cg28785423

<400> 1272
atgtagcaag cccttaatga ctgcaactat tatcataatt agctctgtat g 51

<210> 1273
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1274 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28785423

<400> 1273
ctattatcat aattagctct gtatgacttt ttacattcat cagatccctt a 51

<210> 1274
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<212> DNA
<213> Homo sapiens

<220>
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<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28785423

<400> 1274
ctattatcat aattagctct gtatgctttt tacattcatc agatccctta 50

<210> 1275
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
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<221> misc_feature
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<223> Accession number cg28786600

<400> 1275
ggatgcaccc acgctgggcg cccagcggcc tetaaccgcc gccccagccc a 51

<210> 1276
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1275 is other entry)

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<223> Accession number cg28786600

<400> 1276
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<210> 1277
<211> 51
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<220>
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<223> 1 of 2 allelic variants (1278 is other entry)

<221> misc_feature
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<223> Accession number cg28790405

<400> 1277
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<210> 1278
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<220>
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<223> 2 of 2 allelic variants (1277 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28790405

<400> 1278

ggtatgcttc actaccggg gcgtaccgac gcgacttcga ggaaaacgtg

50

<210> 1279

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1280 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28814812

<400> 1279

taataacagc agagttaccc taagacatac aatctgctgc gtgtatgcta a

51

<210> 1280

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1279 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28814812

<400> 1280

taataacagc agagttaccc taagatatac aatctgctgc gtgtatgcta a

51

<210> 1281

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1282 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28821175

<400> 1281
actattgccca atatttttaa acactaattt gccttttaa ac tagagattta a 51

<210> 1282
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1281 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28821175

<400> 1282
actattgccca atatttttaa acacttattt gccttttaa ac tagagattta a 51

<210> 1283
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1284 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1283
caataaccgc ggtgggtgtg cagcaggaag tttccagta cctgatagcc g 51

<210> 1284
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1283 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1284
caataaccgc ggtgggtgtg cagcaagaag tttccagta cctgatagcc g 51

<210> 1285
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1286 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1285
tgtgcagcag gaagttttcc agtacctgat agccgtcacc ttcgggtgcg t

51

<210> 1286
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1285 is other entry)

<221> misc_feature
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<223> Accession number cg28955364

<400> 1286
tgtgcagcag gaagttttcc agtacttgat agccgtcacc ttcgggtgcg t

51

<210> 1287
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1288 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1287
agccgtcacc ttcgggtgcg ttgatctcgt aatggaatcg agcgtgtca c

51

<210> 1288
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<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1287 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1288
agccgtcacc ttcgggtgcg ttgatgtcgt aatggaatcg agcgctgtca c 51

<210> 1289
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1290 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1289
cagttttgaa tcgcgatggc cttggctacg ggggtagatt tccccttgat a 51

<210> 1290
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1289 is other entry)

<221> misc_feature
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<223> Accession number cg28955364

<400> 1290
cagttttgaa tcgcgatggc cttgggttacg ggggtagatt tccccttgat a 51

<210> 1291
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1292 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg28955364

<400> 1291
tccccttgat aattcgggta gttactccc ctatgtcgga tggaacgttg g 51

<210> 1292
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1291 is other entry)

<221> misc_feature
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<223> Accession number cg28955364

<400> 1292
tccccttgat aattcgggta gttactccc ctatgtcgga tggaacgttg g 51

<210> 1293
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1294 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1293
ttgataattc ggtaggttaa ctcccctatg tcggatggaa cgttggcagg g 51

<210> 1294
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1293 is other entry)

<221> misc_feature
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<223> Accession number cg28955364

<400> 1294
ttgataattc ggtaggttaa ctcccctatg tcggatggaa cgttggcagg g 51

<210> 1295
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1296 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1295
aattcgggta gttactccc ctatgtcggg tggaacggtg gcagggactt c

51

<210> 1296
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1295 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1296
aattcgggta gttactccc ctatgccgga tggaacggtg gcagggactt c

51

<210> 1297
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1298 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1297
actcccctat gtcggatgga acgttggcag ggacttcggt gtacaccgag t

51

<210> 1298
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1297 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1298
actcccctat gtcggatgga acgtagcag ggacttcggt gtacaccgag t 51

<210> 1299
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1300 is other entry)

<221> misc_feature
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<223> Accession number cg28955364

<400> 1299
gggacttcgg tgtacaccga gttatgtggg gtgccggctt tcgcgttattc g 51

<210> 1300
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1299 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1300
gggacttcgg tgtacaccga gttatttggg gtgccggctt tcgcgttattc g 51

<210> 1301
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1302 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg28955364

<400> 1301

acaccgagtt atgtggggtg ccggccttcg cgttatcgaa ggttactgga t

51

<210> 1302

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1301 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28955364

<400> 1302

acaccgagtt atgtggggtg ccggccttcg cgttatcgaa ggttactgga t

51

<210> 1303

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1304 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28955364

<400> 1303

acggaatacc ttcaagtcgt gccatgagtg ccattgacgc cgcgaaatgg a

51

<210> 1304

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1303 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28955364

<400> 1304

acggaatacc ttcaagtcgt gccataagtg ccattgacgc cgcgaaatgg a

51

<210> 1305

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1306 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1305
acgccgcgaa atggatgcaa taaccgcggt ggggtgtgcag caggaagttt t 51

<210> 1306
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1305 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1306
acgccgcgaa atggatgcaa taaccacggt ggggtgtgcag caggaagttt t 51

<210> 1307
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1308 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1307
atggatgcaa taaccgcggt ggggtgtgcag caggaagttt tccagtacct g 51

<210> 1308
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1307 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28955364

<400> 1308
atggatgcaa taaccgcggt ggggtgcgag caggaagttt tccagtacct g 51

<210> 1309
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1310 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28961882

<400> 1309
aacagaatgc aaacaatcaa aaacatagtc catttaaact atctgggcga c 51

<210> 1310
<211> 50
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1309 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg28961882

<400> 1310
aacagaatgc aaacaatcaa aaacaagtcc atttaaacta tctgggcgac 50

<210> 1311
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1312 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28961882

<400> 1311
tggcagttct gctgagattt tttttaggac tttcctgaag cttagcttca 50

<210> 1312
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1311 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28961882

<400> 1312
tggcagttct gctgagattt tttttagga ctttctgaa gcttagcttc a 51

<210> 1313
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1314 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28961882

<400> 1313
acatagtcca tttaaactat ctgggcgaca aaatgggcac ttaattttac t 51

<210> 1314
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1313 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg28961882

<400> 1314
acatagtccta tttaaactat ctgggtgaca aaatgggcac ttaattttac t 51

<210> 1315
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1316 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28970326

<400> 1315
catggcctgt catggcgtag tcttcacgt cgtaaagtat gagacaatcc a 51

<210> 1316
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1315 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28970326

<400> 1316
catggcctgt catggcgtag tcttctacgt cgtaaagtat gagacaatcc a 51

<210> 1317
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1318 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28970326

<400> 1317
gggtccatga ggagttcgtc caaggttcga actcattacc gtcgaatacg

50

<210> 1318
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1317 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28970326

<400> 1318
gggtccatga ggagttcgtc caagggttcg aactcattac cgtcgaatac g

51

<210> 1319
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1320 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28972181

<400> 1319
agctggttct ctccgaaatg catttggtg cagcgtcggg tcattacgtc c

51

<210> 1320
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1319 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28972181

<400> 1320
agctggttct ctccgaaatg catttaggtg cagcgtcggg tcattacgtc c

51

<210> 1321
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1322 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28972181

<400> 1321
aaatgcattt ggggtgcagcg tcgggtcatt acgtcccggg ggtagagcta c 51

<210> 1322
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1321 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28972181

<400> 1322
aaatgcattt ggggtgcagcg tcggggcatt acgtcccggg ggtagagcta c 51

<210> 1323
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1324 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg28972181

<400> 1323
cgggggtaga gctactggat gcttgcgggc ccgtatcggg taccaacagc a 51

<210> 1324
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 2 of 2 allelic variants (1323 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28972181

<400> 1324

cggggtaga gctactggat gcttgagggc ccgtatcggg taccaacagc a

51

<210> 1325

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1326 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28986449

<400> 1325

agggaagagc aagttggtct ggaacacaaa aagggccggg atctcctttg g

51

<210> 1326

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1325 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg28986449

<400> 1326

agggaagagc aagttggtct ggaacgcaaa aagggccggg atctcctttg g

51

<210> 1327

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1328 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29004129

<400> 1327
cgcaagattt cgaggcaact cggtatcact cactgtgctt gaccacgttg g 51

<210> 1328
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1327 is other entry)

<221> misc_feature
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<223> Accession number cg29004129

<400> 1328
cgcaagattt cgaggcaact cggtaccact cactgtgctt gaccacgttg g 51

<210> 1329
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1330 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29012565

<400> 1329
cccattcgga aaatcaatcc gggggcgctg gctgggtag tcacggcggg c 51

<210> 1330
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1329 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29012565

<400> 1330
cccattcgga aaatcaatcc ggggggtgctg gctgggtag tcacggcggg c 51

<210> 1331
<211> 51
<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1332 is other entry)

<221> misc_feature
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<223> Accession number cg29012565

<400> 1331
ggcaaagcca cggttgtccc tcttgaatga gctagattac cctaccctac c 51

<210> 1332
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1331 is other entry)

<221> misc_feature
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<223> Accession number cg29012565

<400> 1332
ggcaaagcca cggttgtccc tcttggatga gctagattac cctaccctac c 51

<210> 1333
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1334 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29141731

<400> 1333
atagggggga tattttgggg tggtagtagt ggtggtctgt tttccagata t 51

<210> 1334
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1333 is other entry)

<221> misc_feature
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<223> Accession number cg29141731

<400> 1334
atagggggga tattttgggg tggtgttagt ggtggtctgt tttccagata t 51

<210> 1335
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1336 is other entry)

<221> misc_feature
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<223> Accession number cg29141731

<400> 1335
aatattcagt aagctttttg aagctcctta cacatccgta aaactttctca g 51

<210> 1336
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1335 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29141731

<400> 1336
aatattcagt aagctttttg aagctactta cacatccgta aaactttctca g 51

<210> 1337
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1338 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29144273

<400> 1337

atgggataag atgtaagttt ttaatactag caatgtacac tactcttttt t

51

<210> 1338

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1337 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29144273

<400> 1338

atgggataag atgtaagttt ttaatgctag caatgtacac tactcttttt t

51

<210> 1339

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1340 is other entry)

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<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

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<222> (0)...(0)

<223> Accession number cg29144339

<400> 1339

aagcaaaacc catcgggggg gggggacatc tacatgccat ctttggtgct

50

<210> 1340

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1339 is other entry)

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<223> Accession number cg29144339

<400> 1340

aagcaaaacc catcgggggg ggggggacat ctacatgcca tctttggtgc t

51

<210> 1341
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (1342 is other entry)

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<400> 1341
ccgctcatag tgctgctcagt cagaatcttc atcattgccg atacgtgata g

51

<210> 1342
<211> 51
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<223> 2 of 2 allelic variants (1341 is other entry)

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ccgctcatag tgctgctcagt cagaaccttc atcattgccg atacgtgata g

51

<210> 1343
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<212> DNA
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<223> 1 of 2 allelic variants (1344 is other entry)

<221> misc_feature
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<400> 1343
ccgccacccc actctaggcc tccctgtggt tcagcatcct caaccccgct t

51

<210> 1344
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (1343 is other entry)

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<223> Accession number cg29202844

<400> 1344
ccgccacccc actctaggcc tccctatggt tcagcatcct caaccccgct t 51

<210> 1345
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<212> DNA
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<223> 1 of 2 allelic variants (1346 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29207528

<400> 1345
cgggtcaggg gcgttcgcgg cgccagctgg cacaacttcg gcaccggcga c 51

<210> 1346
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1345 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29207528

<400> 1346
cgggtcaggg gcgttcgcgg cgccactggc acaacttcgc gaccggcgac 50

<210> 1347
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1348 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29207528

<400> 1347

cttcgacgcc aacgagcttg ccgtagctcc tgatactgac accgtcatcc a

51

<210> 1348

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1347 is other entry)

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<223> Accession number cg29207528

<400> 1348

cttcgacgcc aacgagcttg ccgtaactcc tgatactgac accgtcatcc a

51

<210> 1349

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1350 is other entry)

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<222> (0)...(0)

<223> Accession number cg29207528

<400> 1349

tactgacacc gtcacccagg gagtcgggcc cggcctagcc ctctcgatc c

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<210> 1350

<211> 50

<212> DNA

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<222> (25)...(26)

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<221> misc_feature
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<223> Accession number cg29207528

<400> 1350
tactgacacc gtcattccagg gattcgggccc gccctagccc tcttcgatcc 50

<210> 1351
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<223> 1 of 2 allelic variants (1352 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29207528

<400> 1351
cctcgctcgac acatgccgat aaccgcacag cccaggcatg gcgcgatttc g 51

<210> 1352
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1351 is other entry)

<221> misc_feature
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<223> Accession number cg29207528

<400> 1352
cctcgctcgac acatgccgat aaccgaacag cccaggcatg gcgcgatttc g 51

<210> 1353
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1354 is other entry)

<221> misc_feature
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<223> Accession number cg29207528

<400> 1353
ctgcgcgtcg cagatgccgc acaggcacgg gtcaggggcg ttcgcggcgc c 51

<210> 1354
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1353 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

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<223> Accession number cg29207528

<400> 1354
ctgcgcgtcg cagatgccgc acaggacggg tcaggggcgt tcgcggcgcc

50

<210> 1355
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<223> 1 of 2 allelic variants (1356 is other entry)

<221> misc_feature
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<223> Accession number cg29210581

<400> 1355
tttttcctga gttatggaag gaatggaat tggggaattc aggcttaaaa t

51

<210> 1356
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (1355 is other entry)

<221> misc_feature
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<223> Accession number cg29210581

<400> 1356
tttttcctga gttatggaag gaatgataat tggggaattc aggcttaaaa t

51

<210> 1357

<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1358 is other entry)

<221> misc_feature
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<223> Accession number cg29216983

<400> 1357
gcattctgtg aggctaccgc aggctctggc gtaaagcagt ggagccaggt c 51

<210> 1358
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1357 is other entry)

<221> misc_feature
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<223> Accession number cg29216983

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gcattctgtg aggctaccgc aggctttggc gtaaagcagt ggagccaggt c 51

<210> 1359
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (1360 is other entry)

<221> misc_feature
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<223> Accession number cg29217243

<400> 1359
ggcgcggcgc tccatccaaa tcgatctggg catccgcccc tgtcacgcga a 51

<210> 1360
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 2 of 2 allelic variants (1359 is other entry)

<221> misc_feature
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<223> Accession number cg29217243

<400> 1360
ggcgcggcgc tccatccaaa tcgatttggg catccgcccc tgtcaccgca a 51

<210> 1361
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (1362 is other entry)

<221> misc_feature
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<223> Accession number cg29217243

<400> 1361
cagcaccatt accgacgagc cgagcaccgt ccagataggc ccggcgatcc c 51

<210> 1362
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1361 is other entry)

<221> misc_feature
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<223> Accession number cg29217243

<400> 1362
cagcaccatt accgacgagc cgagcgccgt ccagataggc ccggcgatcc c 51

<210> 1363
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1364 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29217243

<400> 1363
gccgagcacc gtccagatag gcccggcgat cccatgctcc gcagccactg a 51

<210> 1364
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1363 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29217243

<400> 1364
gccgagcacc gtccagatag gcccgacgat cccatgctcc gcagccactg a 51

<210> 1365
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1366 is other entry)

<221> misc_feature
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<223> Accession number cg29217243

<400> 1365
ttcctagatc cgcccaaccg cgacggccag cgtcctcaat gagggttctc g 51

<210> 1366
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1365 is other entry)

<221> misc_feature
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<223> Accession number cg29217243

<400> 1366
ttcctagatc cgcccaaccg cgacgtccag cgtcctcaat gagggttctc g 51

<210> 1367
<211> 51

<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1368 is other entry)

<221> misc_feature
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<223> Accession number cg29217243

<400> 1367
cgcgacggcc agcgctcctca atgagggttc tcggcccggc tgtctctact a 51

<210> 1368
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1367 is other entry)

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<222> (0)...(0)
<223> Accession number cg29217243

<400> 1368
cgcgacggcc agcgctcctca atgagagttc tcggcccggc tgtctctact a 51

<210> 1369
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1370 is other entry)

<221> misc_feature
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<223> Accession number cg29234950

<400> 1369
caaccacagg gcccctctcc gagggtagcc cacaggccac acggtggcga c 51

<210> 1370
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1369 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29234950

<400> 1370

caaccagggg gccctctcc gagggcacc caccaggccac acggtggcga c

51

<210> 1371

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1372 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29237731

<400> 1371

ctcaatcctg acagataccg atcataaggc aatggcactc caggagtatt t

51

<210> 1372

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1371 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29237731

<400> 1372

ctcaatcctg acagataccg atcatgaggc aatggcactc caggagtatt t

51

<210> 1373

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1374 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29237731

<400> 1373
aatcctgaca gataccgatc ataaggcaat ggcactccag gagtatttcc t 51

<210> 1374
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1373 is other entry)

<221> misc_feature
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<223> Accession number cg29237731

<400> 1374
aatcctgaca gataccgatc ataagccaat ggcactccag gagtatttcc t 51

<210> 1375
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1376 is other entry)

<221> misc_feature
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<223> Accession number cg29239003

<400> 1375
ggattccact ttccctgtcc cctacctccc caaactcttg caagaaaata a 51

<210> 1376
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1375 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29239003

<400> 1376
ggattccact ttccctgtcc cctacttccc caaactcttg caagaaaata a 51

<210> 1377
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1378 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29250853

<400> 1377

cgtacgagat cacgttcctc acccagctcc ccaaagacct cacgtgcagc g

51

<210> 1378

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1377 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29250853

<400> 1378

cgtacgagat cacgttcctc acccatctcc ccaaagacct cacgtgcagc g

51

<210> 1379

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1380 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29255997

<400> 1379

aaacaaggaa gagtaggatg gaatcggaat aaaacagtga aagaacatta t

51

<210> 1380

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1379 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29255997

<400> 1380
aaacaaggaa gagtaggatg gaatcgaata aaacagtga agaacattat 50

<210> 1381
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1382 is other entry)

<221> misc_feature
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<223> Accession number cg29255997

<400> 1381
aggatggaat cggaataaaa cagtgaaga acattattct ttgtaccgtg a 51

<210> 1382
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1381 is other entry)

<221> misc_feature
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<223> Accession number cg29255997

<400> 1382
aggatggaat cggaataaaa cagtgaaga acattattct ttgtaccgtg a 51

<210> 1383
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1384 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg29256466

<400> 1383
tgaatataag gctagataat ggagcgtttg tgatcccttg tctattctca g 51

<210> 1384
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1383 is other entry)

<221> misc_feature
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<223> Accession number cg29256466

<400> 1384
tgaatataag gctagataat ggagcatttg tgatcccttg tctattctca g 51

<210> 1385
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1386 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29260975

<400> 1385
ctgcaatgag ctgtgaccac gccactgcac tccagcctgg gcgacagagc a 51

<210> 1386
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1385 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29260975

<400> 1386
ctgcaatgag ctgtgaccac gccaccgcac tccagcctgg gcgacagagc a 51

<210> 1387

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1388 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29260975

<400> 1387

ccagcctggg cgacagagca agaccatgat atttcaagaa aagtccttga g

51

<210> 1388

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1387 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29260975

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ccagcctggg cgacagagca agaccgtgat atttcaagaa aagtccttga g

51

<210> 1389

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1390 is other entry)

<221> misc_feature

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<223> Accession number cg29264501

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51

<210> 1390

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
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<223> 2 of 2 allelic variants (1389 is other entry)

<221> misc_feature
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<400> 1390
ctccccaacc cactccccag taacacaggg ttttccccga ttctcacagt g 51

<210> 1391
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1392 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29337682

<400> 1391
gtggtgcatg cctgtaatcc cagcactttg ggaggctgag gcaggaggat c 51

<210> 1392
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1391 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29337682

<400> 1392
gtggtgcatg cctgtaatcc cagcaatttg ggaggctgag gcaggaggat c 51

<210> 1393
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1394 is other entry)

<221> misc_feature
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<223> Accession number cg29345077

<400> 1393

actcccgacc tcaggtgatc cgcccacctc ggccctcccaa agtgctggga t

51

<210> 1394

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1393 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29345077

<400> 1394

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51

<210> 1395

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<212> DNA

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<223> 1 of 2 allelic variants (1396 is other entry)

<221> misc_feature

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<223> Accession number cg29345273

<400> 1395

cttatggcac gggggctgca gcctggcctc ctctccagg tgggatgcct c

51

<210> 1396

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1395 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29345273

<400> 1396

cttatggcac gggggctgca gcctgcctc ctctccagg tgggatgcct c

51

<210> 1397

<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (1398 is other entry)

<221> misc_feature
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<223> Accession number cg29345769

<400> 1397
ctgtattaag acttaaactc ctgccgcacc tggagtaata aacttgtggg a 51

<210> 1398
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1397 is other entry)

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<223> Accession number cg29345769

<400> 1398
ctgtattaag acttaaactc ctgccacacc tggagtaata aacttgtggg a 51

<210> 1399
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (1400 is other entry)

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<223> Accession number cg29346973

<400> 1399
agttatctca taattaaaaa aaaaaactag ctcgtagaa ttagaatcta a 51

<210> 1400
<211> 50
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<221> misc_feature
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<223> Accession number cg29346973

<400> 1400
agttatctca taattaaaaa aaaaactagc tcgttagaat tagaatctaa 50

<210> 1401
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1402 is other entry)

<221> misc_feature
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<223> Accession number cg29348101

<400> 1401
ccgctcaggc tgctgctgcg ggcgcgctgt ggtactccgc cgaaggcgat a 51

<210> 1402
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1401 is other entry)

<221> misc_feature
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<223> Accession number cg29348101

<400> 1402
ccgctcaggc tgctgctgcg ggcgctgtgt ggtactccgc cgaaggcgat a 51

<210> 1403
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1404 is other entry)

<221> misc_feature
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<223> Accession number cg29348101

<400> 1403
ccgccgaagg cgataagtgg aaggtcgata ccaacggtga caagagcaaa g 51

<210> 1404
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (1403 is other entry)

<221> misc_feature
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<223> Accession number cg29348101

<400> 1404
ccgccgaagg cgataagtgg aaggttgata ccaacggtga caagagcaaa g 51

<210> 1405
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (1406 is other entry)

<221> misc_feature
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<223> Accession number cg29348101

<400> 1405
ataagtggaa ggtcgatacc aacggtgaca agagcaaagt tgttgccgat t 51

<210> 1406
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1405 is other entry)

<221> misc_feature
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<223> Accession number cg29348101

<400> 1406

ataagtggaa ggtcgatacc aacggcgaca agagcaaagt tgttgccgat t

51

<210> 1407

<211> 44

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (1408 is other entry)

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<223> Accession number cg29348101

<400> 1407

cgacgacaag agcgctgtca ctgacccccg ttggagcgac gcgt

44

<210> 1408

<211> 44

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1407 is other entry)

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<222> (0)...(0)

<223> Accession number cg29348101

<400> 1408

cgacgacaag agcgctgtca ctgacgccccg ttggagcgac gcgt

44

<210> 1409

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1410 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29348101

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51

<210> 1410

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (1409 is other entry)

<221> misc_feature
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<223> Accession number cg29348101

<400> 1410
tgctttcttc cgccaagaag gctgctgccca agggcaagta catcctcgga t 51

<210> 1411
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1412 is other entry)

<221> misc_feature
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<223> Accession number cg29348101

<400> 1411
tttctctccgc caagaaggct gccgccaagg gcaagtacat cctcggattt g 51

<210> 1412
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (1411 is other entry)

<221> misc_feature
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<223> Accession number cg29348101

<400> 1412
tttctctccgc caagaaggct gccgctaagg gcaagtacat cctcggattt g 51

<210> 1413
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<223> 1 of 2 allelic variants (1414 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29348230

<400> 1413
tcagaggggtg agaaagccca gagcatttta catgttttagg attttgactt t

51

<210> 1414
<211> 50
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<221> misc_feature
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<223> Accession number cg29348230

<400> 1414
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50

<210> 1415
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<212> DNA
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<220>
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<223> 1 of 2 allelic variants (1416 is other entry)

<221> misc_feature
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<223> Accession number cg29348328

<400> 1415
tgcattacca agagctgacg atctctggag gatcgaatgc cagtcgggca g

51

<210> 1416
<211> 51
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<223> 2 of 2 allelic variants (1415 is other entry)

<221> misc_feature
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<223> Accession number cg29348328

<400> 1416

tgcattacca agagctgacg atctccggag gatcgaatgc cagtcgggca g

51

<210> 1417

<211> 51

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<223> 1 of 2 allelic variants (1418 is other entry)

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<223> Accession number cg29348328

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51

<210> 1418

<211> 51

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<223> 2 of 2 allelic variants (1417 is other entry)

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<223> Accession number cg29348328

<400> 1418

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51

<210> 1419

<211> 51

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<223> 1 of 2 allelic variants (1420 is other entry)

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<223> Accession number cg29348328

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51

<210> 1420

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<223> 2 of 2 allelic variants (1419 is other entry)

<221> misc_feature
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<400> 1420
atgctcggac ggggaaatat cgacgagacc cccattgtca ctcacacttt t 51

<210> 1421
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<223> 1 of 2 allelic variants (1422 is other entry)

<221> misc_feature
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<223> Accession number cg29348328

<400> 1421
tgctcggacg gggaaatatc gacgggaccc ccattgtcac tcacactttt g 51

<210> 1422
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1421 is other entry)

<221> misc_feature
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<223> Accession number cg29348328

<400> 1422
tgctcggacg gggaaatatc gacggaaccc ccattgtcac tcacactttt g 51

<210> 1423
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (1424 is other entry)

<221> misc_feature
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<223> Accession number cg29348328

<400> 1423
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<210> 1424
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<400> 1424
cttttggcct gtcccgagtg accgaagctg ttgacgccgt gcgcgggtcac g 51

<210> 1425
<211> 51
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<400> 1425
gctgttgacg ccgtgcgcgg tcacgccggc gtcaagatcg ctatcgatcc c 51

<210> 1426
<211> 51
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<220>
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<223> 2 of 2 allelic variants (1425 is other entry)

<221> misc_feature
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<400> 1426
gctgttgacg ccgtgcgcgg tcacgtcggc gtcaagatcg ctatcgatcc c 51

<210> 1427
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<223> 1 of 2 allelic variants (1428 is other entry)

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<210> 1428
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<223> 2 of 2 allelic variants (1427 is other entry)

<221> misc_feature
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<400> 1428
ttgacgcggt gcgcggtcac gccggcgtca agatcgctat cgatccccgc c 51

<210> 1429
<211> 51
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<220>
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<223> 1 of 2 allelic variants (1430 is other entry)

<221> misc_feature
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<223> Accession number cg29348328

<400> 1429
gacgcgtgag ttggtttgct gggtttccca agggatcaac gacgaccatc a 51

<210> 1430
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51

<210> 1431
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<223> 1 of 2, allelic variants (1432 is other entry)

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ttatgttatt tataaaacga ccaaggaaat gaatgtaatt tggctttcat a

51

<210> 1432
<211> 51
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<213> Homo sapiens

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<223> 2 of 2 allelic variants (1431 is other entry)

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<400> 1432
ttatgttatt tataaaacga ccaagaaaat gaatgtaatt tggctttcat a

51

<210> 1433
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (1434 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29348993

<400> 1433

gtttgtttgt ttttaactttt tttttttcat tctcgctgta gatagcctga a

51

<210> 1434

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1433 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29348993

<400> 1434

gtttgtttgt ttttaactttt ttttttcatt ctcgctgtag atagcctgaa

50

<210> 1435

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1436 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29348993

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<210> 1436

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<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1435 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29348993

<400> 1436
tttgtttggt ttaacttttt tttttcattc tcgctgtaga tagcctgaat 50

<210> 1437
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1438 is other entry)

<221> misc_feature
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<223> Accession number cg29348993

<400> 1437
tcgctgtaga tagcctgaat ccaaagaaaa ccaaaggagg ttatccaagt a 51

<210> 1438
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<220>
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<223> 2 of 2 allelic variants (1437 is other entry)

<221> misc_feature
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<223> Accession number cg29348993

<400> 1438
tcgctgtaga tagcctgaat ccaaaaaaaaa ccaaaggagg ttatccaagt a 51

<210> 1439
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<220>
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<223> 1 of 2 allelic variants (1440 is other entry)

<221> misc_feature
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<223> Accession number cg29349829

<400> 1439

cataggcacc gcgtgaaggg caccgtaaga atcttcccga atgctcctgt c

51

<210> 1440

<211> 50

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<221> misc_feature

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<223> Accession number cg29349829

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cataggcacc gcgtgaaggg caccgaagaa tcttcccgaa tgctcctgtc

50

<210> 1441

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1442 is other entry)

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<223> Accession number cg29349990

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51

<210> 1442

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1441 is other entry)

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<223> Accession number cg29349990

<400> 1442
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<210> 1443
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1444 is other entry)

<221> misc_feature
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<223> Accession number cg29351920

<400> 1443
tcaggagttt gagaccagcc tggccagcat ggcgaaaccc catctctact a 51

<210> 1444
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (1443 is other entry)

<221> misc_feature
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<223> Accession number cg29351920

<400> 1444
tcaggagttt gagaccagcc tggccggcat ggcgaaaccc catctctact a 51

<210> 1445
<211> 51
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<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1446 is other entry)

<221> misc_feature
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<223> Accession number cg29352964

<400> 1445
ggaaggtgtg cggatactta ttgtcgggtgc ggcacgtcc atccacaccg t 51

<210> 1446
<211> 51
<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1445 is other entry)

<221> misc_feature

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<223> Accession number cg29352964

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51

<210> 1447

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<212> DNA

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<223> 1 of 2 allelic variants (1448 is other entry)

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gccgtcactc cattgatccc cgagtcgga tccatctggc cccacacggc g

51

<210> 1448

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1447 is other entry)

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<223> Accession number cg29352964

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<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (1450 is other entry)

<221> misc_feature
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<400> 1449
ccattgatcc ccgagtccgg atccatctgg cccacacgg cggaaggca a 51

<210> 1450
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<223> 2 of 2 allelic variants (1449 is other entry)

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<223> Accession number cg29352964

<400> 1450
ccattgatcc ccgagtccgg atccacctgg cccacacgg cggaaggca a 51

<210> 1451
<211> 51
<212> DNA
<213> Homo sapiens

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<223> Accession number cg29352964

<400> 1451
cgaccgggta tggctgctc gctcgtcttg cccatattga cgccccgacg c 51

<210> 1452
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1451 is other entry)

<221> misc_feature
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<223> Accession number cg29352964

<400> 1452

cgaccgggta tggctctgctc gctcgccttg cccatattga cgcgccgacg c

51

<210> 1453

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1454 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29352964

<400> 1453

ccccgacgct gctgtcgggtg tgggggagtg acgtttacga ttccccccgg g

51

<210> 1454

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1453 is other entry)

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<223> Accession number cg29352964

<400> 1454

ccccgacgct gctgtcgggtg tggggaagtg acgtttacga ttccccccgg g

51

<210> 1455

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1456 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29354835

<400> 1455

ggggcctttc ctgttgtaga cttcccgtaga ggggtctcaga ccccttgtag a

51

<210> 1456

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1455 is other entry)

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<223> Accession number cg29354835

<400> 1456
ggggcctttc ctgtgtgaca cttcctgtga gggctctcaga ccccttgag a 51

<210> 1457
<211> 51
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<213> Homo sapiens

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<223> 1 of 2 allelic variants (1458 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29357657

<400> 1457
tatccgcggg acgccgcgaa ttcgttcgag accgcacgtt ctacgagggc g 51

<210> 1458
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1457 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29357657

<400> 1458
tatccgcggg acgccgcgaa ttcgtcgcga ccgcacgttc tacgagggcg 50

<210> 1459
<211> 51
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<223> 1 of 2 allelic variants (1460 is other entry)

<221> misc_feature
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<223> Accession number cg29357938

<400> 1459
ttgctatcgc tcgcgctttc gcctctgaac ccaaaatatt gtttgcggat g 51

<210> 1460
<211> 50
<212> DNA
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<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg29357938

<400> 1460
ttgctatcgc tcgcgctttc gcctcgaacc caaaatattg tttgcggatg 50

<210> 1461
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1462 is other entry)

<221> misc_feature
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<223> Accession number cg29360589

<400> 1461
gcccgtgtg acaccattgg tactccggtc cgtctgacct tcgaccaga a 51

<210> 1462
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1461 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29360589

<400> 1462

gcccgtgtg acaccattgg tactcgggtc cgtctgacct tcgacccaga a

51

<210> 1463

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1464 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29360589

<400> 1463

cgatggggcg tgacgaattg cccctgccga cggcgacctc tctggctctg t

51

<210> 1464

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (0)...(0)

<223> Accession number cg29360589

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<210> 1465

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1466 is other entry)

<221> misc_feature
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<223> Accession number cg29363109

<400> 1465
taatccagtg ctcccggctg taccaccctg cctattcaca gtgggcacac t 51

<210> 1466
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1465 is other entry)

<221> misc_feature
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<223> Accession number cg29363109

<400> 1466
taatccagtg ctcccggctg taccaacctg cctattcaca gtgggcacac t 51

<210> 1467
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1468 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29495773

<400> 1467
aggagctgtc cagggttctg gagacgaaac ggagcccgct gggaactgtc c 51

<210> 1468
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1467 is other entry)

<221> misc_feature
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<223> Accession number cg29495773

<400> 1468
aggagctgtc cagggttctg gagactaaac ggagcccgct gggaactgtc c 51

<210> 1469
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1470 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29498780

<400> 1469
agaggagacc acagaagccc cgacgttgca cagccctgca ggcaggggct g 51

<210> 1470
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1469 is other entry)

<221> misc_feature
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<223> Accession number cg29498780

<400> 1470
agaggagacc acagaagccc cgacgctgca cagccctgca ggcaggggct g 51

<210> 1471
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1472 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29513153

<400> 1471
tctcgagaaa aaaaacaacc ggagagactc tagtgaaggt ctcgacaaga c 51

<210> 1472
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1471 is other entry)

<221> misc_feature
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<223> Accession number cg29513153

<400> 1472
tctcgagaaa aaaaacaacc ggagaaactc tagtgaaggt ctcgacaaga c 51

<210> 1473
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1474 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29513153

<400> 1473
gcggcaggaa cctgccactc ctgggagcaa aaagctgctc tcgggaaccc t 51

<210> 1474
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (1473 is other entry)

<221> misc_feature
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<223> Accession number cg29513153

<400> 1474
gcggcaggaa cctgccactc ctgggggcaa aaagctgctc tcgggaaccc t 51

<210> 1475
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1476 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg29514688

<400> 1475
gtagttagg tanggacggg gtttcgccat gttgccagg ctggtcttga a 51

<210> 1476
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1475 is other entry)

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<222> (0)...(0)
<223> Accession number cg29514688

<400> 1476
gtagttagg tanggacggg gtttcacccat gttgccagg ctggtcttga a 51

<210> 1477
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1478 is other entry)

<221> misc_feature
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<223> Accession number cg29514688

<400> 1477
gggtttcgcc atgttgccca ggctggtctt gaactcctgg gctcgagtga t 51

<210> 1478
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1477 is other entry)

<221> misc_feature
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<223> Accession number cg29514688

<400> 1478
gggtttcgcc atgttgccca ggctggtctt gaactcctgg gctcgagtga t 51

<210> 1479
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1480 is other entry)

<221> misc_feature
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<223> Accession number cg29514688

<400> 1479
cttgaactcc tgggctcgag tgatccacct gcctcagcct cccaatgcgc t 51

<210> 1480
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1479 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29514688

<400> 1480
cttgaactcc tgggctcgag tgatctacct gcctcagcct cccaatgcgc t 51

<210> 1481
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1482 is other entry)

<221> misc_feature
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<223> Accession number cg29689883

<400> 1481
ggccactttt ctttttcttg ttttgttttt tttttctttt tttctttttt t 51

<210> 1482
<211> 50
<212> DNA
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<220>

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<221> misc_feature
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<221> misc_feature
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<223> Accession number cg29689883

<400> 1482
ggccactttt ctttttcttg ttttgttttt ttttcttttt ttcttttttt 50

<210> 1483
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1484 is other entry)

<221> misc_feature
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<223> Accession number cg29689883

<400> 1483
tttttttctt tttttctttt tttttcttct tctttttgag acattctcac t 51

<210> 1484
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1483 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29689883

<400> 1484
tttttttctt tttttctttt tttttcttct ctttttgaga cattctcact 50

<210> 1485
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1486 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29692482

<400> 1485
tttctctccac ctccctccac tcattcaggt caggcatcga atgtcacttt c 51

<210> 1486
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1485 is other entry)

<221> misc_feature
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<223> Accession number cg29692482

<400> 1486
tttctctccac ctccctccac tcatttaggt caggcatcga atgtcacttt c 51

<210> 1487
<211> 44
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (19)...(0)
<223> 1 of 2 allelic variants (1488 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29694531

<400> 1487
ttgcaaaaat aacccttgg ggctctgtct cctcaacta ttgc 44

<210> 1488
<211> 43
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (19)...(0)
<223> 2 of 2 allelic variants (1487 is other entry)

<221> misc_feature
<222> (18)...(19)
<223> Nucleotide deleted between bases 18 and 19

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29694531

<400> 1488
ttgcaaaaat aacccttgg gctctgtctc cctcaactat tgc

43

<210> 1489
<211> 47
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (22)...(0)
<223> 1 of 2 allelic variants (1490 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29694531

<400> 1489
ttgcaaaaat aacccttgg ggctctgtct cctcaacta ttgtct

47

<210> 1490
<211> 46
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (22)...(0)
<223> 2 of 2 allelic variants (1489 is other entry)

<221> misc_feature
<222> (21)...(22)
<223> Nucleotide deleted between bases 21 and 22

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29694531

<400> 1490
ttgcaaaaat aacccttgg gctctgtctc cctcaactat tgcct

46

<210> 1491
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 1 of 2 allelic variants (1492 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29694613

<400> 1491

agtaggtatc cccgctcccc caccaacccc caatttgaat gcacatttga

50

<210> 1492

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1491 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29694613

<400> 1492

agtaggtatc cccgctcccc caccacaccc ccaatttgaa tgcacatttg a

51

<210> 1493

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1494 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29694613

<400> 1493

tccagtgttt ttcagtaggt atccccgctc cccacaccaac cccaatttg a

51

<210> 1494

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1493 is other entry)

<221> misc_feature
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<223> Accession number cg29694613

<400> 1494
tccagtgttt ttcagtaggt atccctgctc cccaccaac cccaatttg a

51

<210> 1495
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1496 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29694879

<400> 1495
gttgacagag c

51

<210> 1496
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1495 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg29694879

<400> 1496
gttgacagag c

51

<210> 1497
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1498 is other entry)

<221> misc_feature
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<223> Accession number cg29970826

<400> 1497
gtttgtcctg gcacgaaca ggagacatac gtaagcagct aagtctcttc c

51

<210> 1498

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1497 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29970826

<400> 1498

gtttgtcctg gcacggaaca ggagatatac gtaagcagct aagtctcttc c

51

<210> 1499

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1500 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg29970826

<400> 1499

ctaagtctct tccaaggaac ggtggagaca ccaatcacca tgtcgaggtg a

51

<210> 1500

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1499 is other entry)

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<222> (0)...(0)

<223> Accession number cg29970826

<400> 1500

ctaagtctct tccaaggaac ggtggggaca ccaatcacca tgtcgaggtg a

51

<210> 1501

<211> 51

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1502 is other entry)

<221> misc_feature
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<223> Accession number cg30123222

<400> 1501
ctatgacatg acactattac attttggttt ttagcatttt taaagaggaa g 51

<210> 1502
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1501 is other entry)

<221> misc_feature
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<223> Accession number cg30123222

<400> 1502
ctatgacatg acactattac attttagttt ttagcatttt taaagaggaa g 51

<210> 1503
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1504 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30144940

<400> 1503
cccgcggaca agtcaagatc tgtgatttgg cgtcagtggc aacctagttg 50

<210> 1504
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 2 of 2 allelic variants (1503 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30144940

<400> 1504
cccgcggaca agtcaagatc tgtgattttg gcgtcagtgg caacctagtt g 51

<210> 1505
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1506 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30144940

<400> 1505
catccatcgc gacgtcaaac cgaccgatat cttgggtcaac acccgcggaac a 51

<210> 1506
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1505 is other entry)

<221> misc_feature
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<223> Accession number cg30144940

<400> 1506
catccatcgc gacgtcaaac cgaccaatat cttgggtcaac acccgcggaac a 51

<210> 1507
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<210> 1508
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atgacagaaa tgctacagta agggacagga gatgggggaa ggcaaaaggg g 51

<210> 1509
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<212> DNA
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<223> 1 of 2 allelic variants (1510 is other entry)

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<400> 1509
agtaaggagg agggatggg ggaaggcaaa aggggggttc tacttattaa g 51

<210> 1510
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<400> 1510
agtaaggagg agggatggg ggaagacaaa aggggggttc tacttattaa g 51

<210> 1511
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<212> DNA
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ggagatgggg gaaggcaaaa ggggggttcct acttattaag tcaaatagat c

51

<210> 1512
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<221> misc_feature
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ggagatgggg gaaggcaaaa ggggggttcct acttattaag tcaaatagat c

51

<210> 1513
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<212> DNA
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<223> 1 of 2 allelic variants (1514 is other entry)

<221> misc_feature
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<400> 1513
tatgtgaagt aaaacaaaaa caaaagttgt tacaattttt tcccttctaa t

51

<210> 1514
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1513 is other entry)

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<223> Accession number cg30154402

<400> 1514

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51

<210> 1515

<211> 51

<212> DNA

<213> Homo sapiens

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<223> Accession number cg30177428

<400> 1515

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<210> 1516

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (0)...(0)

<223> Accession number cg30177428

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<210> 1517

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<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1518 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30179644

<400> 1517
ccttttggtgg ggagaagtga aaaaagagga tctgaagact cattagttgt 50

<210> 1518
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<221> misc_feature
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<223> Accession number cg30179644

<400> 1518
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<210> 1519
<211> 51
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<223> 1 of 2 allelic variants (1520 is other entry)

<221> misc_feature
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<223> Accession number cg30275403

<400> 1519
gtgggcagca ggaattgga ggaggaggtg ggggtggggc acagagcggg g 51

<210> 1520
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<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (1519 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg30275403

<400> 1520

gtgggcagca ggaattggga ggaggggtgg ggggtggggca cagagcgggg

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<210> 1521

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (1522 is other entry)

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<223> Accession number cg30373246

<400> 1521

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51

<210> 1522

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1521 is other entry)

<221> misc_feature

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<223> Accession number cg30373246

<400> 1522

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51

<210> 1523

<211> 51

<212> DNA

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1524 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg30386365

<400> 1523
gaccccgatt aggcagctca gggtattatt gcagcttgat ggcacctggg a 51

<210> 1524
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> 2 of 2 allelic variants (1523 is other entry)

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<223> Accession number cg30386365

<400> 1524
gaccccgatt aggcagctca gggtactatt gcagcttgat ggcacctggg a 51

<210> 1525
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<400> 1525
aggcttcacc tcctcagtgg gctagatgca attctaacca gggggcaagt t 51

<210> 1526
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<223> 2 of 2 allelic variants (1525 is other entry)

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<223> Accession number cg30386365

<400> 1526
aggcttcacc tcctcagtgg gctaggtgca attctaacca gggggcaagt t 51

<210> 1527
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<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1528 is other entry)

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<222> (0)...(0)

<223> Accession number cg30420313

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51

<210> 1528

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1527 is other entry)

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<223> Accession number cg30420313

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<210> 1529

<211> 51

<212> DNA

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<220>

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<223> 1 of 2 allelic variants (1530 is other entry)

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<222> (0)...(0)

<223> Accession number cg30421261

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<210> 1530

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1529 is other entry)

<221> misc_feature
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<223> Accession number cg30421261

<400> 1530
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51

<210> 1531
<211> 51
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<223> 1 of 2 allelic variants (1532 is other entry)

<221> misc_feature
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<223> Accession number cg30421963

<400> 1531
aggcactgtc ccttgtcgcc ttcccagaca acctgtaccc tccaggccac c

51

<210> 1532
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (1531 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30421963

<400> 1532
aggcactgtc ccttgtcgcc ttcccggaca acctgtaccc tccaggccac c

51

<210> 1533
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (1534 is other entry)

<221> misc_feature
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<223> Accession number cg30453852

<400> 1533

cggtgcttg attcctttga tgaaaaggca aagccttgaa cctaagtcac c

51

<210> 1534

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1533 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg30453852

<400> 1534

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51

<210> 1535

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1536 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg30489596

<400> 1535

aataagtata gcaagtttat aaaggaaaaa gataaaatac agttccagta t

51

<210> 1536

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1535 is other entry)

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<222> (0)...(0)

<223> Accession number cg30489596

<400> 1536

aataagtata gcaagtttat aaaggaaaaa gataaaatac agttccagta t

51

<210> 1537

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1538 is other entry)

<221> misc_feature
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<223> Accession number cg30489596

<400> 1537
gcctttaatc ctgggagata aagccaagat ctctgagttc aaggccagca t 51

<210> 1538
<211> 51
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<223> 2 of 2 allelic variants (1537 is other entry)

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<223> Accession number cg30489596

<400> 1538
gcctttaatc ctgggagata aagccgagat ctctgagttc aaggccagca t 51

<210> 1539
<211> 51
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1540 is other entry)

<221> misc_feature
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<223> Accession number cg30490648

<400> 1539
acaggtacag cctgcggtca gacacaacca caaggcacat gaactcccca g 51

<210> 1540
<211> 51
<212> DNA
<213> Homo sapiens

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<221> misc_feature
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<223> Accession number cg30490648

<400> 1540
acaggtacag cctgcggtca gacacgacca caaggcacat gaactcccca g 51

<210> 1541
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (1542 is other entry)

<221> misc_feature
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<223> Accession number cg30575906

<400> 1541
ttttctggt aaatggtcct aaaatgaaac ctggcggttta acatggacac t 51

<210> 1542
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (1541 is other entry)

<221> misc_feature
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<223> Accession number cg30575906

<400> 1542
ttttctggt aaatggtcct aaaataaaac ctggcggttta acatggacac t 51

<210> 1543
<211> 51
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1544 is other entry)

<221> misc_feature
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<223> Accession number cg30578763

<400> 1543
gaggtctggt tcgggttgcg catgtgaggg gcaagaggtg tctgccccct c 51

<210> 1544
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1543 is other entry)

<221> misc_feature
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<223> Accession number cg30578763

<400> 1544
gaggtctggt tcgggttcgc catgtaagg gcaagaggtg tctgccccct c 51

<210> 1545
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1546 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30630643

<400> 1545
gttcttggct gggggttagga tgactgcaag aattgggtct gtatttaata a 51

<210> 1546
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (1545 is other entry)

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<223> Accession number cg30630643

<400> 1546
gttcttggct gggggttagga tgactccaag aattgggtct gtatttaata a 51

<210> 1547
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1548 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30748852

<400> 1547
aaccagggaa cattatggcc tgaggcccca gaggagtggg acagttaccc a 51

<210> 1548
<211> 50
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (1547 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30748852

<400> 1548
aaccagggaa cattatggcc tgaggcccgaggagtggga cagttaccca 50

<210> 1549
<211> 51
<212> DNA
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<220>
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<223> Accession number cg30749846

<400> 1549
ggtcgagcag ggttttactt ttagttggat ctgtcgtgtg acttgccctc a 51

<210> 1550
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<223> 2 of 2 allelic variants (1549 is other entry)

<221> misc_feature
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<223> Accession number cg30749846

<400> 1550
ggtcgagcag ggttttactt ttagtgggat ctgtcgtgtg acttgctct a 51

<210> 1551
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<212> DNA
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<223> 1 of 2 allelic variants (1552 is other entry)

<221> misc_feature
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<223> Accession number cg30750319

<400> 1551
ggcttactcc ttgatggaa agtggggaca aaaggctaga gtgcagcagt t 51

<210> 1552
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1551 is other entry)

<221> misc_feature
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<400> 1552
ggcttactcc ttgatggaa agtggagaca aaaggctaga gtgcagcagt t 51

<210> 1553
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<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1554 is other entry)

<221> misc_feature
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<223> Accession number cg30750319

<400> 1553
agcatcagtg gtgccccga cccaggcctt gccacccag aacagatagg a 51

<210> 1554
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<213> Homo sapiens

<220>
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<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30750319

<400> 1554
agcatcagtg gtgccccga cccagccttg ccacccaga acagatagga 50

<210> 1555
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1556 is other entry)

<221> misc_feature
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<223> Accession number cg30750659

<400> 1555
aggactaaat gtaagagaga gggatagcaa agcttgagga aaagaaactc c 51

<210> 1556
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1555 is other entry)

<221> misc_feature
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<223> Accession number cg30750659

<400> 1556

aggactaaat gtaagagaga gggatggcaa agcttgagga aaagaaactc c

51

<210> 1557

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1558 is other entry)

<221> misc_feature

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<223> Accession number cg30750659

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taggaccca tgcctcaaat cgctcaacac ccattccctga ctctgaaaat c

51

<210> 1558

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1557 is other entry)

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<223> Accession number cg30750659

<400> 1558

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51

<210> 1559

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1560 is other entry)

<221> misc_feature

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<223> Accession number cg30783885

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51

<210> 1560

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature
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<223> Accession number cg30783885

<400> 1560
gcggcccaga accttgggcc cggctgctca ctggggcatt ggctgcatac c 51

<210> 1561
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<223> 1 of 2 allelic variants (1562 is other entry)

<221> misc_feature
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<223> Accession number cg30783885

<400> 1561
aaccttgggc cggctactc actggggcat tggctgcata cctgaccac g 51

<210> 1562
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1561 is other entry)

<221> misc_feature
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<400> 1562
aaccttgggc cggctactc actggagcat tggctgcata cctgaccac g 51

<210> 1563
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1564 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30784771

<400> 1563
tttatttcta tagaacaaaa aaaaaagtta agagattagt agagacgggt c 51

<210> 1564
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1563 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30784771

<400> 1564
tttatttcta tagaacaaaa aaaaagttaa gagattagta gagacgggtc 50

<210> 1565
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1566 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30785174

<400> 1565
cgtttctctg gtttttctgg tctccgaaat tcaaggattt ctacagttag c 51

<210> 1566
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1565 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg30785174

<400> 1566

cgttttctctg gtttttctgg tctccaaaat tcaaggattt ctacagttag c

51

<210> 1567

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1568 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg30785603

<400> 1567

aagttcccct agctgagaac caaagaagtg gtcccgactg tgcaggcagc t

51

<210> 1568

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1567 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg30785603

<400> 1568

aagttcccct agctgagaac caaagagtgg tcccgactgt gcaggcagct

50

<210> 1569

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1570 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg30785603

<400> 1569
agttccccta gctgagaacc aaagaagtgg tcccgactgt gcaggcagct t 51

<210> 1570
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1569 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30785603

<400> 1570
agttccccta gctgagaacc aaagagtggg cccgactgtg caggcagctt 50

<210> 1571
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1572 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30785603

<400> 1571
caaagaagtg gtcccgactg tgcaggcagc ttgaaagaag aaacaggccc g 51

<210> 1572
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1571 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30785603

<400> 1572
caaagaagtg gtcccgactg tgcagccagc ttgaaagaag aaacaggccc g 51

<210> 1573
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1574 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30785957

<400> 1573
ttcgcgaaatg tgtgtgtggc atacctggc cccatcgctc gtcccataat c

51

<210> 1574
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1573 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30785957

<400> 1574
ttcgcgaaatg tgtgtgtggc atacctggc cccatcgctc gtcccataat c

51

<210> 1575
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1576 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30786264

<400> 1575
ctcaaaccct ttgaactcct cagtgggtcc ctcccccatg cagctgtact c

51

<210> 1576
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1575 is other entry)

<221> misc_feature
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<223> Accession number cg30786264

<400> 1576
ctcaaaccct ttgaactcct cagtgattcc ctcccccatg cagctgtact c 51

<210> 1577
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1578 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30786450

<400> 1577
tcacagcagc caattctttc tcccttagcc tcacgcggtt ccagtcagcc t 51

<210> 1578
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1577 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30786450

<400> 1578
tcacagcagc caattctttc tccctcagcc tcacgcggtt ccagtcagcc t 51

<210> 1579
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1580 is other entry)

<221> misc_feature

<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg30787589

<400> 1579
cgtctggagc cttctttttt tttttgagac aggatctcgc tccgtcctcc 50

<210> 1580
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1579 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30787589

<400> 1580
cgtctggagc cttctttttt tttttgaga caggatctcg ctccgtcctc c 51

<210> 1581
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1582 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30787589

<400> 1581
cgtctggagc cttctttttt tttttgagac aggatctcgc tccgtcctcc 50

<210> 1582
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1581 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30787589

<400> 1582
cgtctggagc cttctttttt ttttttgaga caggatctcg ctccgtcctc c 51

<210> 1583
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1584 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30787705

<400> 1583
gagtaacacc ctttttcaaa aaaaaagtta ccattttctg taataggaaa a 51

<210> 1584
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1583 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30787705

<400> 1584
gagtaacacc ctttttcaaa aaaaagttac cattttctgt aataggaaaa 50

<210> 1585
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1586 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg30787705

<400> 1585
aaatgtgaaa gactctttag gacaaaatac caagtggaaa gaacaggaat a 51

<210> 1586
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1585 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30787705

<400> 1586
aaatgtgaaa gactctttag gacaatatac caagtggaaa gaacaggaat a 51

<210> 1587
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1588 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30787816

<400> 1587
taaaaacatc actcttggag ctgcagggaa aaggagttga gaagcatgga a 51

<210> 1588
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1587 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30787816

<400> 1588
taaaaacatc actcttggag ctgcatggaa aaggagttga gaagcatgga a 51

<210> 1589
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1590 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30788422

<400> 1589
gattgcatgg aggcccgcc cccccaacc aattctttga taatagcaca g

51

<210> 1590
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1589 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30788422

<400> 1590
gattgcatgg aggcccgcc cccccaacca attctttgat aatagcacag

50

<210> 1591
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1592 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30788717

<400> 1591
atcatatcat gaaagctatc ataaaggaag aaaaataggg atttgactat c

51

<210> 1592
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1591 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30788717

<400> 1592
atcatatcat gaaagctatc ataatgaag aaaaataggg atttgactat c

51

<210> 1593
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1594 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30790895

<400> 1593
gtcctgggca ggaagatgag gcaaacacaa gcacatggat gcacgcacac a

51

<210> 1594
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1593 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30790895

<400> 1594
gtcctgggca ggaagatgag gcaaatacaa gcacatggat gcacgcacac a

51

<210> 1595
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 1 of 2 allelic variants (1596 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg30790895

<400> 1595

caggaagatg aggcaaacac aagcacatgg atgcacgcac acactcgtgc t

51

<210> 1596

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1595 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg30790895

<400> 1596

caggaagatg aggcaaacac aagcaaatgg atgcacgcac acactcgtgc t

51

<210> 1597

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1598 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg30792591

<400> 1597

ttggatattg gctttaaaat gttttcattt aataccccct cccccacaca c

51

<210> 1598

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1597 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg30792591

<400> 1598
ttggatattg gctttaaaat gtttttattt aataccccct cccccacaca c 51

<210> 1599
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1600 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30793374

<400> 1599
aattgaactg ctgttccttg tgtgccgggc cccatagcta gcactgggaa c 51

<210> 1600
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1599 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30793374

<400> 1600
aattgaactg ctgttccttg tgtgctgggc cccatagcta gcactgggaa c 51

<210> 1601
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1602 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg30794324

<400> 1601
tcctaaatga gtgttttagaa tagttatttc attggaaaca aggtcaaaac a 51

<210> 1602
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1601 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg30794324

<400> 1602

tcctaaatga gtgttttagaa tagttgtttc attggaaaca aggtcaaaac a

51

<210> 1603

<211> 45

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1604 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg30794324

<400> 1603

tctaccacaa ttatttgatc aactagttat caaccctgac tgcag

45

<210> 1604

<211> 45

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1603 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg30794324

<400> 1604

tctaccacaa ttatttgatc aactaattat caaccctgac tgcag

45

<210> 1605

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1606 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32073644

<400> 1605
accctcctgg cacatctctg ctcaccctgc gagcaaccga ccccgacgtg g

51

<210> 1606
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1605 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32073644

<400> 1606
accctcctgg cacatctctg ctcactctgc gagcaaccga ccccgacgtg g

51

<210> 1607
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1608 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32119723

<400> 1607
tggatcgcca gggctacggc cagatcaagg tggtcgcgc cgatggggac a

51

<210> 1608
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1607 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32119723

<400> 1608

tggatcgcca gggctacggc cagattaagg tggccgcgc cgatggggac a

51

<210> 1609

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1610 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32119813

<400> 1609

gcccgtcgta cgtggggcgc tcgcgctggg tgcagacgcg cttgattggt t

51

<210> 1610

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1609 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32119813

<400> 1610

gcccgtcgta cgtggggcgc tcgcggtggg tgcagacgcg cttgattggt t

51

<210> 1611

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1612 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32120097

<400> 1611

tggcctgcac gtccgcacg ctcagctccc gctggccccg gctgtacagg a

51

<210> 1612

<211> 50

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1611 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32120097

<400> 1612
tggcctgcac gtcccgcacg ctcagtcccg ctggccccgg ctgtacagga 50

<210> 1613
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1614 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32126043

<400> 1613
cctgtggcat ccgttctgat ggaaacgtgc agttgtattt ggaagttcag a 51

<210> 1614
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1613 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32126043

<400> 1614
cctgtggcat ccgttctgat ggaaatgtgc agttgtattt ggaagttcag a 51

<210> 1615
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1616 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32149436

<400> 1615
agggcgcccc gagtggctcc aggaacgacg gaaaccctc agggcttttg g 51

<210> 1616
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1615 is other entry)

<221> misc_feature
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<400> 1616
agggcgcccc gagtggctcc aggaaggacg gaaaccctc agggcttttg g 51

<210> 1617
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1618 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32149517

<400> 1617
tgtgctgta tgtgcgttg ctctgcatgc gtggtgtgtg tatgtgtgtg 50

<210> 1618
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 2 of 2 allelic variants (1617 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32149517

<400> 1618

tgtgcgtgta tgtgcgcttg ctctgtcatg cgtgggtgtgt gtatgtgtgt g

51

<210> 1619

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1620 is other entry)

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<222> (0)...(0)

<223> Accession number cg32149517

<400> 1619

tgggtggtgtc gccagagagt gacctgcctg tctgggggtgg aggaaaagcc a

51

<210> 1620

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1619 is other entry)

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<222> (0)...(0)

<223> Accession number cg32149517

<400> 1620

tgggtggtgtc gccagagagt gacctccctg tctgggggtgg aggaaaagcc a

51

<210> 1621

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1622 is other entry)

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<222> (0)...(0)

<223> Accession number cg32150747

<400> 1621
cagaacttcg gcagtaaaga ataaaaggcc agacagagag gcagcagcac a 51

<210> 1622
<211> 50
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (1621 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32150747

<400> 1622
cagaacttcg gcagtaaaga ataaaggcca gacagagagg cagcagcaca 50

<210> 1623
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1624 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32152942

<400> 1623
cacagctgtg catgtcgact taggtggcct gccagctcat ctccggcggc a 51

<210> 1624
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1623 is other entry)

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<223> Accession number cg32152942

<400> 1624
cacagctgtg catgtcgact taggtagcct gccagctcat ctccggcggc a 51

<210> 1625
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1626 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32152942

<400> 1625
ggtggcctgc cagctcatct ccggcggcac ggtcaacgac gtcgagctgc c 51

<210> 1626
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1625 is other entry)

<221> misc_feature
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<223> Accession number cg32152942

<400> 1626
ggtggcctgc cagctcatct ccggcagcac ggtcaacgac gtcgagctgc c 51

<210> 1627
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1628 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32152942

<400> 1627
ggcctgccag ctcctctccg gcggcacggt caacgacgac gagctgccgc g 51

<210> 1628
<211> 51
<212> DNA
<213> Homo sapiens

<220> .
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<223> 2 of 2 allelic variants (1627 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32152942

<400> 1628
ggcctgccag ctcacatctcgc gcggcccggc caacgacgac gagctgccgc g 51

<210> 1629
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1630 is other entry)

<221> misc_feature
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<223> Accession number cg32152942

<400> 1629
tcacttggtc agattggcca tggatagtc cctgatcccc aacgatgtgg g 51

<210> 1630
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1629 is other entry)

<221> misc_feature
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<223> Accession number cg32152942

<400> 1630
tcacttggtc agattggcca tggatgtgca cctgatcccc aacgatgtgg g 51

<210> 1631
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1632 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg32152942

<400> 1631
ggccatggat agtcacctga tccccaacga tgtgggctag ctgactagcg g 51

<210> 1632
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1631 is other entry)

<221> misc_feature
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<223> Accession number cg32152942

<400> 1632
ggccatggat agtcacctga tccccgacga tgtgggctag ctgactagcg g 51

<210> 1633
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1634 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32152942

<400> 1633
tcacctgatc cccaacgatg tgggctagct gactagcggt aacttgagct c 51

<210> 1634
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1633 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32152942

<400> 1634
tcacctgatc cccaacgatg tgggccagct gactagcggt aacttgagct c 51

<210> 1635
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1636 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32152942

<400> 1635
cgcgatcctc gttgaggcgc tgaagacgct gggatgcagc acgaaactcc g 51

<210> 1636
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1635 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32152942

<400> 1636
cgcgatcctc gttgaggcgc tgaaggcgcct gggatgcagc acgaaactcc g 51

<210> 1637
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1638 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32153241

<400> 1637
accgggctcc ggtcccgagg tccacagca gttgaccagg catgggccgc a 51

<210> 1638
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1637 is other entry)

<221> misc_feature
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<223> Accession number cg32153241

<400> 1638
accgggtcc ggtcccgagg tcccatagca gttgaccagg catgggccgc a 51

<210> 1639
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1640 is other entry)

<221> misc_feature
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<223> Accession number cg32153241

<400> 1639
gcatgggccg cagggctgcc agcgcgacag ctcgtaccgc gtgcttggtg a 51

<210> 1640
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1639 is other entry)

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<223> Accession number cg32153241

<400> 1640
gcatgggccg cagggctgcc agcgcaacag ctcgtaccgc gtgcttggtg a 51

<210> 1641
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1642 is other entry)

<221> misc_feature
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<223> Accession number cg32153241

<400> 1641

cagctcgtag cgcggtgcttg gtgataagtc cgtcgtgggc gaaatgctcc t

51

<210> 1642

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1641 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32153241

<400> 1642

cagctcgtag cgcggtgcttg gtgatgagtc cgtcgtgggc gaaatgctcc t

51

<210> 1643

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1644 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32153241

<400> 1643

tggtgataag tccgtcgtgg gcgaaatgct cctcggccag gccgggggta c

51

<210> 1644

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1643 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32153241

<400> 1644

tggtgataag tccgtcgtgg gcgaagtgct cctcggccag gccgggggta c

51

<210> 1645

<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1646 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32158391

<400> 1645
tgcataccat gctccagagg aagcagataa atctgaccc t aaacctgggg t 51

<210> 1646
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1645 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32158391

<400> 1646
tgcataccat gctccagagg aagcaataaa tctgaccta aacctgggg t 50

<210> 1647
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1648 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32168122

<400> 1647
catgcgcgct ggcctccatg ggtggcgga cgcactgtg gacgcacttg c 51

<210> 1648
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1647 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32168122

<400> 1648

catgcgcgct ggcctccatg ggtgggggga ccgactgtgt gacgcacttg c

51

<210> 1649

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1650 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32168828

<400> 1649

tgattcgccg cacaggtcgt ttagggcaac gccaaagttcg aagacgtccc c

51

<210> 1650

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1649 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32168828

<400> 1650

tgattcgccg cacaggtcgt ttaggacaac gccaaagttcg aagacgtccc c

51

<210> 1651

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1652 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32177197

<400> 1651
caccgtgttg ccgaaaaggt cgctcacctc taccacgata cggtgggtac c 51

<210> 1652
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1651 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32177197

<400> 1652
caccgtgttg ccgaaaaggt cgctcgctc taccacgata cggtgggtac c 51

<210> 1653
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1654 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32177197

<400> 1653
ggggaaggaa tggaaagcgg tggggtcgta ggtcgtcggg gcagtgcacc a 51

<210> 1654
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (1653 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32177197

<400> 1654

ggggaaggaa tggaaagcgg tggggccgtc ggtcgtcggg gcagtgcgcc a

51

<210> 1655

<211> 45

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (20)...(0)

<223> 1 of 2 allelic variants (1656 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32177584

<400> 1655

ccgcacgcgt gagccaccgt gcctggccca cgtgacactg ttaaa

45

<210> 1656

<211> 45

<212> DNA

<213> Homo sapiens

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<222> (20)...(0)

<223> 2 of 2 allelic variants (1655 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32177584

<400> 1656

ccgcacgcgt gagccaccgc gcctggccca cgtgacactg ttaaa

45

<210> 1657

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1658 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32180618

<400> 1657

aatcagcacg gtgcgcgtga ggggcgggcg cgcttctcac acatgctgtg c

51

<210> 1658

<211> 51

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1657 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32180618

<400> 1658
aatcagcacg gtgcgcgtga ggggcaggcg cgcttctcac acatgctgtg c 51

<210> 1659
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1660 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32195480

<400> 1659
cctttccctt gcgtacactc tggactccag gcaggaaaat caaggcctca c 51

<210> 1660
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1659 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32195480

<400> 1660
cctttccctt gcgtacactc tggaccccag gcaggaaaat caaggcctca c 51

<210> 1661
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1662 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32195480

<400> 1661
gcattagtcc aggacagcag acccctctgg acgctgactc gggatggggt 50

<210> 1662
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1661 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32195480

<400> 1662
gcattagtcc aggacagcag acccctctg gacgctgact cgggatgggg t 51

<210> 1663
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (1664 is other entry)

<221> misc_feature
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<223> Accession number cg32308743

<400> 1663
tttccgtacg cgtgaacgtc tgtgttgtct gtggaatccc ctggggacgt t 51

<210> 1664
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1663 is other entry)

<221> misc_feature
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<223> Accession number cg32308743

<400> 1664

tttccgtacg cgtgaacgtc tgtgtcgtct gtggaatccc ctcgggacgt t

51

<210> 1665

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1666 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32338390

<400> 1665

gagccataag ggaggacttg gcagcgtgct tgctccctga gtgacgttgt g

51

<210> 1666

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1665 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32338390

<400> 1666

gagccataag ggaggacttg gcagcatgct tgctccctga gtgacgttgt g

51

<210> 1667

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1668 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg32544064

<400> 1667

caggagtcca tgaccagcct ggccaacaca gtgagacccc gtctctacta a

51

<210> 1668

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1667 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32544064

<400> 1668
caggagttca tgaccagcct ggccagcaca gtgagacccc gtctctacta a 51

<210> 1669
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1670 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32544064

<400> 1669
gagttcatga ccagcctggc caacacagtg agaccccgtc tctactaaaa a 51

<210> 1670
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1669 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg32544064

<400> 1670
gagttcatga ccagcctggc caacatagtg agaccccgtc tctactaaaa a 51

<210> 1671
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 1 of 2 allelic variants (1672 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg33193895

<400> 1671
tctctcctnt gccaaagataa aaataatatt ctocctgggc tttcttaact a 51

<210> 1672
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1671 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg33193895

<400> 1672
tctctcctnt gccaaagataa aaatatattc tcocctgggct ttcttaacta 50

<210> 1673
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1674 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg33193895

<400> 1673
tctcctntgc caagataaaa ataatatctt ccctgggctt tcttaactac a 51

<210> 1674
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1673 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg33193895

<400> 1674
tctcctntgc caagataaaa ataatttctc cctgggcttt cttaactaca 50

<210> 1675
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1676 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg33194116

<400> 1675
gtgtcactag tgtgaaaaaa gttgtagtgg agagcttggt atgtcaggca a 51

<210> 1676
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1675 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg33194116

<400> 1676
gtgtcactag tgtgaaaaaa gttgtgtgga gagcttggtgta tgtcaggcaa 50

<210> 1677
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1678 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg33199608

<400> 1677
gattctcctg tctcaacctg ccaagtagct gggactacag gcgcacgccca c 51

<210> 1678
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1677 is other entry)

<221> misc_feature
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<223> Accession number cg33199608

<400> 1678
gattctcctg tctcaacctg ccaagcagct gggactacag gcgcacgccca c 51

<210> 1679
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1680 is other entry)

<221> misc_feature
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<223> Accession number cg33199608

<400> 1679
cgccaccacg accggccaat ttctgcactt ttagtagaga cagggcttca c 51

<210> 1680
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1679 is other entry)

<221> misc_feature
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<223> Accession number cg33199608

<400> 1680
cgccaccacg accggccaat ttctgtactt ttagtagaga cagggcttca c 51

<210> 1681
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1682 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg33208319

<400> 1681
ccttgatgag gctgtctttt aagctcaatt gaaggtagta acaacaatcc t 51

<210> 1682
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1681 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg33208319

<400> 1682
ccttgatgag gctgtctttt aagcttaatt gaaggtagta acaacaatcc t 51

<210> 1683
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1684 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg33208319

<400> 1683
gaaatgtgta gattctggaa cagtgccctag caggttgcag atacttacta g 51

<210> 1684
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1683 is other entry)

<221> misc_feature
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<400> 1684
gaaatgtgta gattctggaa cagtgtctag caggttgcag atacttacta g

51

<210> 1685
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1686 is other entry)

<221> misc_feature
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<223> Accession number cg33208319

<400> 1685
aagttttctg agtgaatgaa aagtcacaaa tgaatgtatc cttccaagca t

51

<210> 1686
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1685 is other entry)

<221> misc_feature
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<223> Accession number cg33208319

<400> 1686
aagttttctg agtgaatgaa aagtcgaaaa tgaatgtatc cttccaagca t

51

<210> 1687
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1688 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg33265890

<400> 1687

tcgtgcttgg aatcagcagg cagggccact tccctcttga agtcacatc t

51

<210> 1688

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1687 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg33265890

<400> 1688

tcgtgcttgg aatcagcagg cagggccactt ccctcttgaa gtcacatct

50

<210> 1689

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> 1 of 2 allelic variants (1690 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg33271693

<400> 1689

gttcgggaga aagctacgac caagtacgcc cagctcgggc cttagaactt c

51

<210> 1690

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1689 is other entry)

<221> misc_feature
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<221> misc_feature
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<223> Accession number cg33271693

<400> 1690
gttcgggaga aagctacgac caagtcgccc agctcgggcc ttagaacttc 50

<210> 1691
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1692 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg33899283

<400> 1691
cccttcggga ttggagtctg acctgaaagc atggataatt attcacattt c 51

<210> 1692
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1691 is other entry)

<221> misc_feature
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<223> Accession number cg33899283

<400> 1692
cccttcggga ttggagtctg acctgtaagc atggataatt attcacattt c 51

<210> 1693
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1694 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg34078594

<400> 1693

agagacaagg cttcctcata ggacggcaga gccaccttta ggaacagctt g

51

<210> 1694

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1693 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg34078594

<400> 1694

agagacaagg cttcctcata ggacgcagag ccacctttag gaacagcttg

50

<210> 1695

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (1696 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg34078594

<400> 1695

tcaaagtga gaagcaggag gcggggagtt ccgcctctcc cagcccaagg g

51

<210> 1696

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1695 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg34078594

<400> 1696
tcaaagtgaa gaagcaggag gcgggcagtt ccgcctctcc cagcccaagg g 51

<210> 1697
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1698 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34078713

<400> 1697
tgaaaatagt gtgctgagcc ctggaacatt aaaaatgtgt tcctatgtgg a 51

<210> 1698
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1697 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34078713

<400> 1698
tgaaaatagt gtgctgagcc ctggagcatt aaaaatgtgt tcctatgtgg a 51

<210> 1699
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1700 is other entry)

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<222> (0)...(0)
<223> Accession number cg34096681

<400> 1699
agacttgaaa acaactggaa gagagggttc ctcaaggag aagacacgag a 51

<210> 1700
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1699 is other entry)

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<222> (0)...(0)

<223> Accession number cg34096681

<400> 1700

agacttgaaa acaactggaa gagagagttc ctcaagggag aagacacgag a

51

<210> 1701

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1702 is other entry)

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<222> (0)...(0)

<223> Accession number cg34098766

<400> 1701

ctcagcctca tgagtagctg ggacagcaga catgtacaac cacacctggc t

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<210> 1702

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1701 is other entry)

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<400> 1702

ctcagcctca tgagtagctg ggacacagac atgtacaacc acacctggct

50

<210> 1703

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1704 is other entry)

<221> misc_feature
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<223> Accession number cg34098766

<400> 1703
acacctggct aatttttttt ttttttggg gtggaaatag aatctcactg a 51

<210> 1704
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1703 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34098766

<400> 1704
acacctggct aatttttttt ttttttgggg tggaaataga atctcactga 50

<210> 1705
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> 1 of 2 allelic variants (1706 is other entry)

<221> misc_feature
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<223> Accession number cg34098766

<400> 1705
cacctggcta attttttttt ttttttgggg tggaaataga atctcactga t 51

<210> 1706
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1705 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg34098766

<400> 1706
cacctggcta attttttttt tttttggggt ggaaatagaa tctcactgat . 50

<210> 1707
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1708 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34107938

<400> 1707
cacaaatgct ctgtaggcac gtgtggctag tgactgccct acggtcggca t 51

<210> 1708
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1707 is other entry)

<221> misc_feature
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<223> Accession number cg34107938

<400> 1708
cacaaatgct ctgtaggcac gtgtgactag tgactgccct acggtcggca t 51

<210> 1709
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1710 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34108088

<400> 1709
atattaacca ttgaatgaag tatgggtatc ctccctctt ttttgataat c 51

<210> 1710
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1709 is other entry)

<221> misc_feature
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<223> Accession number cg34108088

<400> 1710
atattaacca ttgaatgaag tatgggtatc ctccctctt ttttgataat c 51

<210> 1711
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1712 is other entry)

<221> misc_feature
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<223> Accession number cg34126415

<400> 1711
atgctaggaa gctagctcct ggggggttca gatctagtga gggtagcctt c 51

<210> 1712
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1711 is other entry)

<221> misc_feature
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<223> Accession number cg34126415

<400> 1712

atgctaggaa gctagctcct gggggattca gatctagtga ggggtgccttt c

51

<210> 1713

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1714 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg34126415

<400> 1713

aagtaaaaac aaacaagata actttttttt ttctgagatg aattttcact t

51

<210> 1714

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1713 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg34126415

<400> 1714

aagtaaaaac aaacaagata acttttctttt ttctgagatg aattttcact t

51

<210> 1715

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1716 is other entry)

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<222> (0)...(0)

<223> Accession number cg34147197

<400> 1715

ggctcaagca atcctccgcg ctcagtctcc caagcagctg ggactacagg c

51

<210> 1716

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<221> misc_feature
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<223> Accession number cg34147197

<400> 1716
ggctcaagca atcctcccg ctcagcctcc caagcagctg ggactacagg c 51

<210> 1717
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1718 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34387835

<400> 1717
tgtattttta gtagagatgg ggttttacca tgtgggcctg gcaggtctcg a 51

<210> 1718
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1717 is other entry)

<221> misc_feature
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<223> Accession number cg34387835

<400> 1718
tgtattttta gtagagatgg ggtttcacca tgtgggcctg gcaggtctcg a 51

<210> 1719
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1720 is other entry)

<221> misc_feature
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<223> Accession number cg34387835

<400> 1719
cctcggcctc ccaaattcct gggactacag gcgtgagcca ctgcaccgg c

51

<210> 1720
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1719 is other entry)

<221> misc_feature
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<223> Accession number cg34387835

<400> 1720
cctcggcctc ccaaattcct gggaccacag gcgtgagcca ctgcaccgg c

51

<210> 1721
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1722 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34387835

<400> 1721
accggtgcgt gccaccacac ccgaccaatt tttgtatttt tagtagagat g

51

<210> 1722
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1721 is other entry)

<221> misc_feature
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<223> Accession number cg34387835

<400> 1722
accggtgcgt gccaccacac ccgactaatt tttgtatttt tagtagagat g

51

<210> 1723
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1724 is other entry)

<221> misc_feature
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<223> Accession number cg34387835

<400> 1723
tgccaccaca cccgaccaat ttttgcattt ttagtagaga tgggggttta c

51

<210> 1724
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (1723 is other entry)

<221> misc_feature
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<400> 1724
tgccaccaca cccgaccaat ttttgcattt ttagtagaga tgggggttta c

51

<210> 1725
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1726 is other entry)

<221> misc_feature
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<221> misc_feature
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taaacttcga tctttccctg tgctcaacat tctatttgg atcccggtct

50

<210> 1726

<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (1725 is other entry)

<221> misc_feature
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<223> Accession number cg34390673

<400> 1726
taaacttcga tctttccctg tgctctaaca ttcctatttg gatcccggtc t 51

<210> 1727
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<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1728 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34405904

<400> 1727
agttcgctgt tgattgctat aattttctct ctaaaatctg gattttcatc t 51

<210> 1728
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1727 is other entry)

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<222> (0)...(0)
<223> Accession number cg34405904

<400> 1728
agttcgctgt tgattgctat aattttctctc taaaatctgg attttcatct 50

<210> 1729
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<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1730 is other entry)

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<222> (0)...(0)

<223> Accession number cg34407516

<400> 1729

cacatatatc tcaacaaacc atgcacatca tctgttcaga actgggaaac g

51

<210> 1730

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1729 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg34407516

<400> 1730

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51

<210> 1731

<211> 51

<212> DNA

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1732 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg34407558

<400> 1731

ccaagctcct gcctcgcaat tgcctttgta ggccaagatc atgccgtgaa g

51

<210> 1732

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1731 is other entry)

<221> misc_feature
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<223> Accession number cg34407558

<400> 1732
ccaagctcct gcctcgcaat tgcctctgta ggccaagatc atgccgtgaa g 51

<210> 1733
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<223> 1 of 2 allelic variants (1734 is other entry)

<221> misc_feature
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<223> Accession number cg34407558

<400> 1733
caagatcatg ccgtgaagtg gcctttccta gctaacttt tgetttttga t 51

<210> 1734
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1733 is other entry)

<221> misc_feature
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<400> 1734
caagatcatg ccgtgaagtg gcctttccta gctaacttt tgetttttga t 51

<210> 1735
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<223> 1 of 2 allelic variants (1736 is other entry)

<221> misc_feature
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<400> 1735

tcctagccta acttttgctt ttgatgcat actccagtc caaaacttcc t

51

<210> 1736

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (1735 is other entry)

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<223> Accession number cg34407558

<400> 1736

tcctagccta acttttgctt ttgatgcat actccagtc caaaacttcc t

51

<210> 1737

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1738 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg34407558

<400> 1737

ggccaaaatc gtcgtgaagt caccctctgc aggccatgct cctgcgtccg a

51

<210> 1738

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1737 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg34407558

<400> 1738

ggccaaaatc gtcgtgaagt caccactgc aggccatgct cctgcgtccg a

51

<210> 1739

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1740 is other entry)

<221> misc_feature
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<223> Accession number cg34407558

<400> 1739
cgtcgtgaag tcaccctctg caggcctagc tcctgcgtcc gagtgctgtg t 51

<210> 1740
<211> 51
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<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1739 is other entry)

<221> misc_feature
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<400> 1740
cgtcgtgaag tcaccctctg caggcctagc tcctgcgtcc gagtgctgtg t 51

<210> 1741
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1742 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34407558

<400> 1741
caccctctgc aggcctagct cctgcgtccg agtgctgtgt aggccaagct a 51

<210> 1742
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1741 is other entry)

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<223> Accession number cg34407558

<400> 1742
caccctctgc aggccctagct cctgcctccg agtgctgtgt aggccaagct a 51

<210> 1743
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1744 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34407558

<400> 1743
ctctgcaggc ctagctcctg cgtccgagtg ctgtgtaggc caagctaata c 51

<210> 1744
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1743 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34407558

<400> 1744
ctctgcaggc ctagctcctg cgtccaagtg ctgtgtaggc caagctaata c 51

<210> 1745
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1746 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34407558

<400> 1745
aagctaatagc ctcacagcac acttttgagg ctgagcggtt ccttttgtgc a 51

<210> 1746
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1745 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34407558

<400> 1746
aagctaattgc ctcacagcac actttcgagg ctgagcggtt ccttttgtgc a 51

<210> 1747
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1748 is other entry)

<221> misc_feature
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<223> Accession number cg34407558

<400> 1747
tcacagcaca cttttgaggc tgagcggttc cttttgtgca tcctctccaa g 51

<210> 1748
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1747 is other entry)

<221> misc_feature
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<223> Accession number cg34407558

<400> 1748
tcacagcaca cttttgaggc tgagcatttc cttttgtgca tcctctccaa g 51

<210> 1749
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1750 is other entry)

<221> misc_feature
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<223> Accession number cg34407558

<400> 1749
caagccctga acttactcca gttggcctct ccagaccaag ctctccctcc c 51

<210> 1750
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1749 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34407558

<400> 1750
caagccctga acttactcca gttggctctet ccagaccaag ctctccctcc c 51

<210> 1751
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1752 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34409256

<400> 1751
ttactatata tgatgtagtc taataatttt ctatctatt ttatttcctt t 51

<210> 1752
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1751 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg34409256

<400> 1752
ttactatata tgatgtagtc taatactttt ctatcctatt ttatttcctt t 51

<210> 1753
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1754 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34409256

<400> 1753
tatatatgat gtagtctaata aattttctat cctattttat ttcctttttt t 51

<210> 1754
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1753 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34409256

<400> 1754
tatatatgat gtagtctaata aattttctatc ctattttatt ttcctttttt 50

<210> 1755
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1756 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34411960

<400> 1755
atggtggaga tgcttctggt ttattctgtg gctaccgctg ttactgcttg g 51

<210> 1756
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1755 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34411960

<400> 1756
atggtggaga tgcttctggt ttatttctgtg gctaccgctg ttactgcttg g 51

<210> 1757
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1758 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34664360

<400> 1757
agctagacat agagccctga ccgtgtgatt ccaactgtgg aattcacaca a 51

<210> 1758
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> 2 of 2 allelic variants (1757 is other entry)

<221> misc_feature
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<223> Accession number cg34664360

<400> 1758
agctagacat agagccctga ccgtgcgatt ccaactgtgg aattcacaca a 51

<210> 1759
<211> 51

<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1760 is other entry)

<221> misc_feature
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<223> Accession number cg34750113

<400> 1759
ttttattggt ttgagacaga gtctcactct gttgcctagg ctggagtgcg g

51

<210> 1760
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1759 is other entry)

<221> misc_feature
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<400> 1760
ttttattggt ttgagacaga gtctcgctct gttgcctagg ctggagtgcg g

51

<210> 1761
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1762 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg34750113

<400> 1761
ggctggagtg cagtgggtgcg atcacagctc actgcaactt ccacctctg g

51

<210> 1762
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1761 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg34750113

<400> 1762

ggctggagtg cagtgggtgca atcacggctc actgcaactt ccacctcctg g

51

<210> 1763

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1764 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg34888218

<400> 1763

aaatgttggg atcaatatct aaatcgaact ccaaattaca gcctccaggg a

51

<210> 1764

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1763 is other entry)

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<222> (0)...(0)

<223> Accession number cg34888218

<400> 1764

aaatgttggg atcaatatct aaatcaaact ccaaattaca gcctccaggg a

51

<210> 1765

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1766 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg34888218

<400> 1765
caggctgtat gcctgaagtc cccaagtacc aagtgcattgt actctgctct g 51

<210> 1766
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1765 is other entry)

<221> misc_feature
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<223> Accession number cg34888218

<400> 1766
caggctgtat gcctgaagtc cccaaatacc aagtgcattgt actctgctct g 51

<210> 1767
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1768 is other entry)

<221> misc_feature
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<223> Accession number cg34888218

<400> 1767
gaagtcacca agtaccaagt gcatgtactc tgctctgggc taaggatgaa a 51

<210> 1768
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1767 is other entry)

<221> misc_feature
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<223> Accession number cg34888218

<400> 1768
gaagtcacca agtaccaagt gcatgcactc tgctctgggc taaggatgaa a 51

<210> 1769
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1770 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg34896418

<400> 1769

aaacaaggat taaatctggt cctggtggtt gtatgggata aacatggatt t

51

<210> 1770

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1769 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg34896418

<400> 1770

aaacaaggat taaatctggt cctggcggtt gtatgggata aacatggatt t

51

<210> 1771

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1772 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35001967

<400> 1771

tgagcagaga aactgacct ggtttggcag ggacaggaga tacgctgggt t

51

<210> 1772

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1771 is other entry)

<221> misc_feature
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<223> Accession number cg35001967

<400> 1772
tgagcagaga acactgacct ggttttgcag ggacaggaga tacgctgggt t 51

<210> 1773
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (1774 is other entry)

<221> misc_feature
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<223> Accession number cg35001967

<400> 1773
agcagagaac actgacctgg tttggcaggg acaggagata cgctggggtt g 51

<210> 1774
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1773 is other entry)

<221> misc_feature
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<223> Accession number cg35001967

<400> 1774
agcagagaac actgacctgg tttggtaggg acaggagata cgctggggtt g 51

<210> 1775
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1776 is other entry)

<221> misc_feature
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<223> Accession number cg35001967

<400> 1775

agatacgctg ggttggtatg gatcagcaag aggggtactgc taatgggaac a

51

<210> 1776

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1775 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35001967

<400> 1776

agatacgctg ggttggtatg gatcaacaag aggggtactgc taatgggaac a

51

<210> 1777

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1778 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35001967

<400> 1777

aatgggaaca gggagggaag gctcaacccc attcccgat ttcctgatt c

51

<210> 1778

<211> 50

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1777 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35001967

<400> 1778

aatgggaaca gggagggaag gctcacccca ttcccgatt tccctgattc

50

<210> 1779

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1780 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35003947

<400> 1779

tggtctggtg aatgggaact taacatgtct ttgccgttac atattcttg a

51

<210> 1780

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1779 is other entry)

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<222> (0)...(0)

<223> Accession number cg35003947

<400> 1780

tggtctggtg aatgggaact taacacgtct ttgccgttac atattcttg a

51

<210> 1781

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1782 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35003951

<400> 1781

ttgaactcct gacctcaagt gatccaccg cctcagcctc ctaaagtgt g

51

<210> 1782

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1781 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35003951

<400> 1782
ttgaactcct gacctcaagt gatccgcccg cctcagcctc ctaaagtgct g 51

<210> 1783
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1784 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35013956

<400> 1783
cagaatccag ccctgcttga tgcaatcctc ttcagccagg cgttcctgaa t 51

<210> 1784
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1783 is other entry)

<221> misc_feature
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<223> Accession number cg35013956

<400> 1784
cagaatccag ccctgcttga tgcaaccctc ttcagccagg cgttcctgaa t 51

<210> 1785
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1786 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg35014502

<400> 1785

gagcagtttc tgtttttcta gttaagatgt actgcacatc cccctactgt t

51

<210> 1786

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1785 is other entry)

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<223> Accession number cg35014502

<400> 1786

gagcagtttc tgtttttcta gttaatatgt actgcacatc cccctactgt t

51

<210> 1787

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1788 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35017611

<400> 1787

gcaggcagac gggcagggcc agaggcgcta cgggggtctc ctgcactgta t

51

<210> 1788

<211> 50

<212> DNA

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1787 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35017611

<400> 1788
gcaggcagac gggcagggcc agagggtac cggggtctcc tgcactgtat 50

<210> 1789
<211> 51
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<220>
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<223> 1 of 2 allelic variants (1790 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35019280

<400> 1789
ataaactgtg tcagacatgg gcgacgcggg gaccgctgga gggaggcgcg c 51

<210> 1790
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1789 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg35019280

<400> 1790
ataaactgtg tcagacatgg gcgaccggg accgctggag ggaggcgcg 50

<210> 1791
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (1792 is other entry)

<221> misc_feature
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<223> Accession number cg35019280

<400> 1791
tccgctggga gcaggagggg cggggccggg cttgaggagt ggctggccgc c 51

<210> 1792
<211> 50
<212> DNA
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<223> 2 of 2 allelic variants (1791 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

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<400> 1792
tccgctggga gcaggagggg cggggcgggc ttgaggagtg gctggccgcc

50

<210> 1793
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (1794 is other entry)

<221> misc_feature
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<223> Accession number cg35023126

<400> 1793
agaaatacca ttctggacat aagacttggc taaaatttca tgatgaagat a

51

<210> 1794
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1793 is other entry)

<221> misc_feature
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<223> Accession number cg35023126

<400> 1794
agaaatacca ttctggacat aagacgtggc taaaatttca tgatgaagat a

51

<210> 1795

<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1796 is other entry)

<221> misc_feature
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<223> Accession number cg35049067

<400> 1795
tctccctgat ggacggggaa gtcttgtttg tggaagacac tgagccacgc t 51

<210> 1796
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1795 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35049067

<400> 1796
tctccctgat ggacggggaa gtcttctttg tggaagacac tgagccacgc t 51

<210> 1797
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1798 is other entry)

<221> misc_feature
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<223> Accession number cg35049067

<400> 1797
caccaccacc ggcattccggg gaggagtgtc aaacgggtga ctggccagg a 51

<210> 1798
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (1797 is other entry)

<221> misc_feature
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<223> Accession number cg35049067

<400> 1798
caccaccacc ggcacccggg gaggactgtc aaacgggtga ctccggccagg a 51

<210> 1799
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1800 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35049067

<400> 1799
tgcgggcacc ctctcgcggg tggacaatga ggcgcctggga ggccggttgtc c 51

<210> 1800
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1799 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35049067

<400> 1800
tgcgggcacc ctctcgcggg tggacgatga ggcgcctggga ggccggttgtc c 51

<210> 1801
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1802 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35049628

<400> 1801
gctggaggat tgcttgaagc caggaattca agaccagcct gggcaacata g 51

<210> 1802
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1801 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35049628

<400> 1802
gctggaggat tgcttgaagc caggagttca agaccagcct gggcaacata g 51

<210> 1803
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1804 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35063579

<400> 1803
gcagatcact ggaggtcagg agttcaagac cagactggcc aacatggtga a 51

<210> 1804
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1803 is other entry)

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<222> (0)...(0)
<223> Accession number cg35063579

<400> 1804
gcagatcact ggaggtcagg agttcgagac cagactggcc aacatggtga a 51

<210> 1805
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1806 is other entry)

<221> misc_feature
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<223> Accession number cg35066497

<400> 1805
gcgtggcacg cccgtcaggg gcaggtgccc caggggtactc ctacggtgct c 51

<210> 1806
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1805 is other entry)

<221> misc_feature
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<223> Accession number cg35066497

<400> 1806
gcgtggcacg cccgtcaggg gcaggagccc caggggtactc ctacggtgct c 51

<210> 1807
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1808 is other entry)

<221> misc_feature
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<223> Accession number cg35066497

<400> 1807
cccagggtag tctacggtg ctcggtcttc ccaccgtggg agtgccgaga c 51

<210> 1808
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (1807 is other entry)

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<223> Accession number cg35066497

<400> 1808

cccagggtac tcctacggtg ctcggaacttc ccaccgtggg agtgccgaga c

51

<210> 1809

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1810 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35066497

<400> 1809

caccgtggga gtgccgagac actgatcgat gggctcttaca ggtatggcat t

51

<210> 1810

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1809 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35066497

<400> 1810

caccgtggga gtgccgagac actgaccgat gggctcttaca ggtatggcat t

51

<210> 1811

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1812 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35066497

<400> 1811
gggtcttaca ggtatggcat ttacggaca gtgaggaaga tagacgagg a 51

<210> 1812
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1811 is other entry)

<221> misc_feature
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<223> Accession number cg35066497

<400> 1812
gggtcttaca ggtatggcat ttactgaca gtgaggaaga tagacgagg a 51

<210> 1813
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1814 is other entry)

<221> misc_feature
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<223> Accession number cg35066497

<400> 1813
caggtatggc attttacgga cagtgaggaa gatagacgag ggatggcgct c 51

<210> 1814
<211> 51
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<220>
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<223> 2 of 2 allelic variants (1813 is other entry)

<221> misc_feature
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<223> Accession number cg35066497

<400> 1814
caggtatggc attttacgga cagtgggaa gatagacgag ggatggcgct c 51

<210> 1815
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1816 is other entry)

<221> misc_feature

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<223> Accession number cg35066497

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51

<210> 1816

<211> 51

<212> DNA

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<223> Accession number cg35066497

<400> 1816

ggcctgattc ttgatgtcgt cctggcggtc gctgatggcg tccttggcct t

51

<210> 1817

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1818 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35068462

<400> 1817

tggcacagga gcccgagatc ttatttcttg acgagccgac aaatcacctt g

51

<210> 1818

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1817 is other entry)

<221> misc_feature
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<223> Accession number cg35068462

<400> 1818
tggcacagga gcccgagatc ttattccttg acgagccgac aaatcacctt g

51

<210> 1819
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1820 is other entry)

<221> misc_feature
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<223> Accession number cg35072832

<400> 1819
ttttggataa tatgtaactc tccacaatgt cgcttccgta gcaattgtag a

51

<210> 1820
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (1819 is other entry)

<221> misc_feature
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<223> Accession number cg35072832

<400> 1820
ttttggataa tatgtaactc tccactatgt cgcttccgta gcaattgtag a

51

<210> 1821
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (1822 is other entry)

<221> misc_feature
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<223> Accession number cg35074019

<400> 1821

tgcagaagga actggactcg ctgcagggag agaaagtaca cctgaaggag a

51

<210> 1822

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1821 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35074019

<400> 1822

tgcagaagga actggactcg ctgcatggag agaaagtaca cctgaaggag a

51

<210> 1823

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1824 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35097790

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51

<210> 1824

<211> 51

<212> DNA

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1823 is other entry)

<221> misc_feature

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<223> Accession number cg35097790

<400> 1824

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51

<210> 1825

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1826 is other entry)

<221> misc_feature
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<223> Accession number cg35097892

<400> 1825
gtattttcag tagagacggg gttttacat gttggccagg ctggtctcga a 51

<210> 1826
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1825 is other entry)

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<223> Accession number cg35097892

<400> 1826
gtattttcag tagagacggg gttttgccat gttggccagg ctggtctcga a 51

<210> 1827
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1828 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35098722

<400> 1827
tatgtcttct ttcgttggtt agtggcttgc aggatatttt gacgagcata a 51

<210> 1828
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1827 is other entry)

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<223> Accession number cg35098722

<400> 1828
tatgtcttct ttcggttggt agtgggttgc aggatatttt gagcagcata a 51

<210> 1829
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1830 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35098722

<400> 1829
ctttcggttg ttagtggctt gcaggatatt ttgagcagca taaaactggt a 51

<210> 1830
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1829 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35098722

<400> 1830
ctttcggttg ttagtggctt gcagggtatt ttgagcagca taaaactggt a 51

<210> 1831
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1832 is other entry)

<221> misc_feature
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<223> Accession number cg35106817

<400> 1831
atgcaggtgc cgggtgagga cggcaccatg ccgaaactgt tcggacggat c 51

<210> 1832
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1831 is other entry)

<221> misc_feature
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<223> Accession number cg35106817

<400> 1832
atgcaggtgc cgggtgagga cggcatcatg ccgaaactgt tcggacggat c 51

<210> 1833
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1834 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35111750

<400> 1833
atattggatc tttccctggt tttttgtat ctacgagacc ttcattggtta t 51

<210> 1834
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1833 is other entry)

<221> misc_feature
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<221> misc_feature
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<223> Accession number cg35111750

<400> 1834
atattggatc tttccctggt tttttgtatc tagcagacct tcattggttat 50

<210> 1835

<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1836 is other entry)

<221> misc_feature
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<223> Accession number cg35137271

<400> 1835
agccaatggt gcacagtgat gatacgaatg tcaatctttg ctcggtcagt g 51

<210> 1836
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1835 is other entry)

<221> misc_feature
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<223> Accession number cg35137271

<400> 1836
agccaatggt gcacagtgat gatacaaatg tcaatctttg ctcggtcagt g 51

<210> 1837
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1838 is other entry)

<221> misc_feature
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<223> Accession number cg35137271

<400> 1837
ttgctcggtc agtgaggatg tcgccctgac ccttctgct cccagaaag g 51

<210> 1838
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1837 is other entry)

<221> misc_feature
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<223> Accession number cg35137271

<400> 1838
ttgctcggtc agtgaggatg tcgccttgac ccttcctgct ccccagaaag g 51

<210> 1839
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1840 is other entry)

<221> misc_feature
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<223> Accession number cg35138283

<400> 1839
tgaagtataa gaatattctg ctgctgttga gtggtatgta atgtatatgt c 51

<210> 1840
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1839 is other entry)

<221> misc_feature
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<223> Accession number cg35138283

<400> 1840
tgaagtataa gaatattctg ctgcttttga gtggtatgta atgtatatgt c 51

<210> 1841
<211> 45
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1842 is other entry)

<221> misc_feature
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<223> Accession number cg35138283

<400> 1841
gttttataca ttattgaaag tggaatatta gattctacca ctagt 45

<210> 1842
<211> 45
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (1841 is other entry)

<221> misc_feature
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<223> Accession number cg35138283

<400> 1842
gttttataca ttattgaaag tggaacatta gattctacca ctagt 45

<210> 1843
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1844 is other entry)

<221> misc_feature
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<223> Accession number cg35350458

<400> 1843
ttctcgtcta gcagtattca gataccctt ctgctcagcc tgcttggcgt t 51

<210> 1844
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1843 is other entry)

<221> misc_feature
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<223> Accession number cg35350458

<400> 1844
ttctcgtcta gcagtattca gatactcctt ctgctcagcc tgcttggcgt t 51

<210> 1845
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1846 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35354409

<400> 1845
ttttccggag ttatttaaaa aaaaaacaaa cagatgcctt ttaagggtta t 51

<210> 1846
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35354409

<400> 1846
ttttccggag ttatttaaaa aaaaacaaac agatgccttt taagggttat 50

<210> 1847
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1848 is other entry)

<221> misc_feature
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<223> Accession number cg35364749

<400> 1847
cccatcacca acgccaccct ggaccgggtg agtgcctggg ctagccctgt c 51

<210> 1848
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1847 is other entry)

<221> misc_feature
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<223> Accession number cg35364749

<400> 1848
cccatcacca acgccaccct ggaccaggtg agtgccctggg ctagccctgt c 51

<210> 1849
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (1850 is other entry)

<221> misc_feature
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<223> Accession number cg35364849

<400> 1849
gttgatgctt gatttaagag taagtgttat cgtgttcagt tttatatct c 51

<210> 1850
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1849 is other entry)

<221> misc_feature
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<223> Accession number cg35364849

<400> 1850
gttgatgctt gatttaagag taagtattat cgtgttcagt tttatatct c 51

<210> 1851
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (1852 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35817789

<400> 1851
ctcttagcaa ccaataattt ttttttcaat aattaagtac caatttcctg c 51

<210> 1852
<211> 50
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (1851 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35817789

<400> 1852
ctcttagcaa ccaataattt tttttcaata attaagtacc aatttcctgc 50

<210> 1853
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (1854 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35817789

<400> 1853
caatttcctg ctaatgggca ggcccacctt tattttcttt tttttccatt a 51

<210> 1854
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (1853 is other entry)

<221> misc_feature
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<223> Accession number cg35817789

<400> 1854

caatttctg ctaatgggca ggccccctt tatttctttt tttttccatt a

51

<210> 1855

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1856 is other entry)

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<222> (0)...(0)

<223> Accession number cg35817789

<400> 1855

ctaattgggca ggcccacctt tatttctttt tttttccatt agaacgagca t

51

<210> 1856

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1855 is other entry)

<221> misc_feature

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<223> Accession number cg35817789

<400> 1856

ctaattgggca ggcccacctt tatttttttt tttttccatt agaacgagca t

51

<210> 1857

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1858 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35907288

<400> 1857

gaagagcact tgcagccgca tcaggtgaac atcaaactgc aaagccacct g

51

<210> 1858

<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (1857 is other entry)

<221> misc_feature
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<223> Accession number cg35907288

<400> 1858
gaagagcact tgcagccgca tcaggcgaac atcaaactgc aaagccacct g

51

<210> 1859
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1860 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35927209

<400> 1859
cccccttggt agtgggcgca cgaatcagtc ttcttcgcgg tccatggtga c

51

<210> 1860
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1859 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35927209

<400> 1860
cccccttggt agtgggcgca cgaattagtc ttcttcgcgg tccatggtga c

51

<210> 1861
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1862 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35927209

<400> 1861
ccacgggatc accggcatcg cgcagaccga cgaagttaac ccctttaacg a 51

<210> 1862
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1861 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35927209

<400> 1862
ccacgggatc accggcatcg cgcaggccga cgaagttaac ccctttaacg a 51

<210> 1863
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1864 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35927209

<400> 1863
gatcaccggc atcgcgcaga ccgacgaagt taaccctttt aacgaccgcg c 51

<210> 1864
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1863 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35927209

<400> 1864
gatcaccggc atcgcgacaga ccgacaaagt taaccctttt aacgaccgc c 51

<210> 1865
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1866 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35929317

<400> 1865
gccgagcatg gtggcgggca cctgtagtcc cagccacctg ggaggctgag g 51

<210> 1866
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1865 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35929317

<400> 1866
gccgagcatg gtggcgggca cctgtggtcc cagccacctg ggaggctgag g 51

<210> 1867
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1868 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35933276

<400> 1867
atgagttcct gcgataaccc ggtagtctcg aaaatctggg ctccgtata c 51

<210> 1868
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1867 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35933276

<400> 1868
atgagttcct gcgataaccc ggtagcctcg aaaatctggg ctccggtata c 51

<210> 1869
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (1870 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35933276

<400> 1869
cctgcgataa cccggtagtc tcgaaaatct gggctccggt atacgacgag a 51

<210> 1870
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1869 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35933276

<400> 1870
cctgcgataa cccggtagtc tcgaagatct gggctccggt atacgacgag a 51

<210> 1871
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1872 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35933276

<400> 1871

ccggtatacg acgagatagt ggatataccc atcttgctca tcgtcttaag g

51

<210> 1872

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1871 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35933276

<400> 1872

ccggtatacg acgagatagt ggatacaccc atcttgctca tcgtcttaag g

51

<210> 1873

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1874 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35933276

<400> 1873

taaggacgcc cttgccaaga gccttgtaaa cgttatggat agcagtttca g

51

<210> 1874

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1873 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35933276

<400> 1874
taaggacgcc cttgccaaga gccttataaa cgttatggat agcagtttca g 51

<210> 1875
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1876 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35933276

<400> 1875
taaacggttat ggatagcagt ttcaggggtca gtagacaccc acacctcgcg c 51

<210> 1876
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1875 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35933276

<400> 1876
taaacggttat ggatagcagt ttcagagtca gtagacaccc acacctcgcg c 51

<210> 1877
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1878 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35933276

<400> 1877
ctgactcgaa gagcaaatac ggggtgacag ccgaagcacc ataacccatg a 51

<210> 1878
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1877 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35933276

<400> 1878

ctgactcgaa gagcaaatac gggttaacag ccgaagcacc ataaccatg a

51

<210> 1879

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1880 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35933276

<400> 1879

agagcaaata cgggttgaca gccgaagcac cataaccat gaggagggcg a

51

<210> 1880

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1879 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35933276

<400> 1880

agagcaaata cgggttgaca gccgaggcac cataaccat gaggagggcg a

51

<210> 1881

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1882 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35933276

<400> 1881
agcgatctcg gtcaggccga cccctcgat ggcactcgtc gttccggcga a 51

<210> 1882
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1881 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35933276

<400> 1882
agcgatctcg gtcaggccga ccccgcgat ggcactcgtc gttccggcga a 51

<210> 1883
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1884 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35933276

<400> 1883
ccctcgatgc gactcgtcgt tccggcgaag tactcatcaa tgagttcctg c 51

<210> 1884
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1883 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35933276

<400> 1884

ccctcgatgc gactcgctgt tccggtgaag tactcatcaa tgagttcctg c

51

<210> 1885

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1886 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35980513

<400> 1885

aaaatgagcc gggcgtggtg acacacgcct gtagtcccag ctacttgga g

51

<210> 1886

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1885 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg35980513

<400> 1886

aaaatgagcc gggcgtggtg acacatgcct gtagtcccag ctacttgga g

51

<210> 1887

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1888 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg36173201

<400> 1887

gcctccagaa ctgtgagaga ataaacgtcc gatgttttaa gccattcagt t

51

<210> 1888

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1887 is other entry)

<221> misc_feature
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<223> Accession number cg36173201

<400> 1888
gcctccagaa ctgtgagaga ataaatgtcc gatgttttaa gccattcagt t 51

<210> 1889
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1890 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36180692

<400> 1889
gaggactgct tgagcccagg agttcaagac cagcctgggc aacacagtga g 51

<210> 1890
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1889 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36180692

<400> 1890
gaggactgct tgagcccagg agttcgagac cagcctgggc aacacagtga g 51

<210> 1891
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1892 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36190410

<400> 1891
acaggcgtga gccaccatgc ccagccttga atactgaatc taagtatttt t 51

<210> 1892
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1891 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36190410

<400> 1892
acaggcgtga gccaccatgc ccagccttga atactgaatc taagtatttt t 51

<210> 1893
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1894 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36190410

<400> 1893
ccagccttga atactgaatc taagtatttt ttgctagttt taaaataatt a 51

<210> 1894
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1893 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36190410

<400> 1894
ccagccttga atactgaatc taagtatttt ttgctagttt taaaataatt a 51

<210> 1895
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1896 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36190410

<400> 1895
tctagcatat gttaaagtaa gtagattttt tttttaactc tccatttgat a 51

<210> 1896
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1895 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36190410

<400> 1896
tctagcatat gttaaagtaa gtagattttt ttttaactct ccatttgata 50

<210> 1897
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1898 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36504297

<400> 1897
cgttttcttc agtgcttcat tttatactc aaattctgct gaagtgattt a 51

<210> 1898

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1897 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36504297

<400> 1898
cgttttcttc agtgcttcat tttatgcctc aaattctgct gaagtgattt a 51

<210> 1899
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1900 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36517624

<400> 1899
cctcctcgtc gcggaacggg ctctcccga agcgctcctc cagctgccgg c 51

<210> 1900
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1899 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36517624

<400> 1900
cctcctcgtc gcggaacggg ctctcgccga agcgctcctc cagctgccgg c 51

<210> 1901
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 1 of 2 allelic variants (1902 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36517624

<400> 1901
ctgccggcga agcttctggg aactggccca gccaaactct tcaagctgct g 51

<210> 1902
<211> 50
<212> DNA
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<220>
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<221> misc_feature
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<223> Accession number cg36517624

<400> 1902
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<210> 1903
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1904 is other entry)

<221> misc_feature
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<223> Accession number cg36588981

<400> 1903
aggagcacct caaggcctgt gaccgagca ccatgtcggg gtgtggctgc a 51

<210> 1904
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1903 is other entry)

<221> misc_feature
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<223> Accession number cg36588981

<400> 1904
aggagcacct caaggcctgt gacccaagca ccatgtcggg gtgtggctgc a 51

<210> 1905
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1906 is other entry)

<221> misc_feature
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<223> Accession number cg36603177

<400> 1905
tgagatcagg agttcgagac cagcccagcc aacatagtga aaccctgtct c 51

<210> 1906
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1905 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36603177

<400> 1906
tgagatcagg agttcgagac cagcctagcc aacatagtga aaccctgtct c 51

<210> 1907
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1908 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36618790

<400> 1907

caggcacggt ggttcacgtc tgtaacccca gcactttggg aggctgagga a 51

<210> 1908

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> 2 of 2 allelic variants (1907 is other entry)

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<222> (0)...(0)

<223> Accession number cg36618790

<400> 1908

caggcacggt ggttcacgtc tgtaatccca gcactttggg aggctgagga a 51

<210> 1909

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1910 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg36618790

<400> 1909

cagcactttg ggaggctgag gaaggctggat gacttgagcc caggagttag a 51

<210> 1910

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1909 is other entry)

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<222> (0)...(0)

<223> Accession number cg36618790

<400> 1910

cagcactttg ggaggctgag gaaggcggat gacttgagcc caggagttag a 51

<210> 1911

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1912 is other entry)

<221> misc_feature
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<223> Accession number cg36618790

<400> 1911
ctttgggagg ctgaggaagg tggatgactt gagcccagga gtttgagacc a 51

<210> 1912
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1911 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36618790

<400> 1912
ctttgggagg ctgaggaagg tggatcactt gagcccagga gtttgagacc a 51

<210> 1913
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1914 is other entry)

<221> misc_feature
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<223> Accession number cg36618790

<400> 1913
gaaggtggat gacttgagcc caggagtttg agaccagcct gggcaacatg g 51

<210> 1914
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (1913 is other entry)

<221> misc_feature
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<223> Accession number cg36618790

<400> 1914
gaaggtaggat gacttgagcc caggaatttg agaccagcct gggcaacatg g

51

<210> 1915
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1916 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36623778

<400> 1915
tgtgcctatc aaggttgtagg tcgaccgttg gaacgtgcc gtcaccgtca c

51

<210> 1916
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1915 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36623778

<400> 1916
tgtgcctatc aaggttgtagg tcgaccgttg gaacgtgcc gtcaccgtca c

51

<210> 1917
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1918 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36733186

<400> 1917
gctccacagg acaatgacct tggcccgtgg cccatcctct ctggcctcca t

51

<210> 1918
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1917 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36733186

<400> 1918
gctccacagg acaatgacct tggccggtgg cccatcctct ctggcctcca t 51

<210> 1919
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1920 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36753762

<400> 1919
caggagtcca agaccagcct ggccaacatg atgaaaccct gtctctacta a 51

<210> 1920
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1919 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36753762

<400> 1920
caggagtcca agaccagcct ggccagcatg atgaaaccct gtctctacta a 51

<210> 1921
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1922 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36753762

<400> 1921
ctactaaaaa tacacaaagt tagccaggcg tgggtggcacg tgcctgtaat c 51

<210> 1922
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1921 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36753762

<400> 1922
ctactaaaaa tacacaaagt tagccgggcg tgggtggcacg tgcctgtaat c 51

<210> 1923
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1924 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36999717

<400> 1923
cctgcgcctt cggatacgat cagcgtctag aggcatttgg ggccgacggc a 51

<210> 1924
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1923 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg36999717

<400> 1924
cctgcgcctt cggatacgat cagcgcctag aggcatttgg ggccgacggc a 51

<210> 1925
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1926 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36999717

<400> 1925
gtctagaggc atttggggcc gacggcatgc ttagtgccga caacctcacc g 51

<210> 1926
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1925 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg36999717

<400> 1926
gtctagaggc atttggggcc gacggatgct tagtgccgac aacctcacccg 50

<210> 1927
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1928 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg37003369

<400> 1927
gtgagtttca gttgatttaa ggaataaaaa aagaccattt tgctaaacac t 51

<210> 1928
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1927 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg37003369

<400> 1928
gtgagtttca gttgatttaa ggaataaaaa agaccatttt gctaaacact 50

<210> 1929
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1930 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg37028403

<400> 1929
caggtaaccc gcatattggt gctggtggag tgcccaacac ggcacttgga a 51

<210> 1930
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1929 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg37028403

<400> 1930

caggtaaccc gcatattgtt gctggcggag tgcccaacac ggcacttgga a

51

<210> 1931

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1932 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg37056126

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ctggggctca ggcctatga cccaacggcc attggtggcc tgtcctcatg g

51

<210> 1932

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1931 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg37056126

<400> 1932

ctggggctca ggcctatga cccaatggcc attggtggcc tgtcctcatg g

51

<210> 1933

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1934 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg37056126

<400> 1933

caaaccacaa tagcagttct ggggttatggg tttggtaaaa ccacctcagg g

51

<210> 1934

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1933 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg37056126

<400> 1934
caaaccacaa tagcagttct gggttttggg tttggtaaaa ccacctcagg g 51

<210> 1935
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1936 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg37418902

<400> 1935
atccacctca caaagaaatg caacacccat tagcggtcac tctcattctc c 51

<210> 1936
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1935 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg37418902

<400> 1936
atccacctca caaagaaatg caacatccat tagcggtcac tctcattctc c 51

<210> 1937
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1938 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg37418902

<400> 1937
caaagaaatg caacacccat tagcggtcac tctcattctc cttgtccagc c 51

<210> 1938
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1937 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg37418902

<400> 1938
caaagaaatg caacacccat tagcggtcac tctcattctc cttgtccagc c 51

<210> 1939
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (1940 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38034239

<400> 1939
ggcctggaac aggagagcgg gcgtagctcg ggcttctatg aagatcccag c 51

<210> 1940
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (1939 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg38034239

<400> 1940

ggcctggaac aggagagcgg gcgtactcgg gcttctatga agatcccagc

50

<210> 1941

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1942 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38068769

<400> 1941

ttatgtcct catctttcta gattggttca gatgccctt ctaggaagcc t

51

<210> 1942

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1941 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38068769

<400> 1942

ttatgtcct catctttcta gattgattca gatgccctt ctaggaagcc t

51

<210> 1943

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1944 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38068769

<400> 1943

tctagattgg ttcagatgcc ccttctagga agccttccca gattttcgcc c

51

<210> 1944

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1943 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38068769

<400> 1944
tctagattgg ttcagatgcc ccttccagga agccttccca gattttcgcc c 51

<210> 1945
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1946 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38070669

<400> 1945
actggtatgc cactgaaaaa aaaaaacaaa aaaacaaaac ccaaagccaa a 51

<210> 1946
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1945 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38070669

<400> 1946
actggtatgc cactgaaaaa aaaaacaaaa aaacaaaacc caaagccaaa 50

<210> 1947
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1948 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38206730

<400> 1947

agggtgtgccca catgttcatt ttcgggtcaa ggcgtacacg tgcaggtgtg t

51

<210> 1948

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1947 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38206730

<400> 1948

agggtgtgccca catgttcatt ttcgggtcaa ggcgtacacg tgcaggtgtg t

51

<210> 1949

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1950 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38206730

<400> 1949

gttcatttttc ggttcaaggc gtacacgtgc aggtgtgtta cgtgttcatt t

51

<210> 1950

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1949 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38206730

<400> 1950
gttcattttc ggttcaaggc gtacatgtgc aggtgtgtta cgtgttcatt t 51

<210> 1951
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1952 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38276118

<400> 1951
ttttgaaatt agccaaaaaa aaaaatcaaa ccttaaacad tgttcaattc 50

<210> 1952
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1951 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38276118

<400> 1952
ttttgaaatt agccaaaaaa aaaaatcaa accttaaca ttgttcaatt c 51

<210> 1953
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1954 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38277495

<400> 1953

cagcaccttg ggaggctgag gtgggcggat cacctgaggt tgggagttcg a

51

<210> 1954

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1953 is other entry)

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<222> (0)...(0)

<223> Accession number cg38277495

<400> 1954

cagcaccttg ggaggctgag gtgggtggat cacctgaggt tgggagttcg a

51

<210> 1955

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1956 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38278604

<400> 1955

caggaatgtg atagaaagtg gctgggaaga gggagctgag gctggtgggt c

51

<210> 1956

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1955 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38278604

<400> 1956

caggaatgtg atagaaagtg gctggcaaga gggagctgag gctggtgggt c

51

<210> 1957
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (1958 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38279706

<400> 1957
tgcagctcca tggctcaaca aggtgcggat gcctgctgga cctggctgct t 51

<210> 1958
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (1957 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38279706

<400> 1958
tgcagctcca tggctcaaca aggtgtggat gcctgctgga cctggctgct t 51

<210> 1959
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<400> 1959
ccacgtgtca tgactgtctg tccttctcca aggcagcatt cagacacccc g 51

<210> 1960
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<223> 2 of 2 allelic variants (1959 is other entry)

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<400> 1960
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<210> 1961
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<400> 1961
cgccccctc ggccaccaaa aatgctggga ccacaggctg taatttattt t 51

<210> 1962
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<400> 1962
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<210> 1963
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<210> 1964

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<223> 2 of 2 allelic variants (1963 is other entry)

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gcctcggcca ccaaaaatgc tgggatcaca ggctgtaatt tatttttttc a

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<223> 1 of 2 allelic variants (1966 is other entry)

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<210> 1966

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (1965 is other entry)

<221> misc_feature

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<400> 1966

cctcggccac caaaaatgct gggactacag gctgtaattt atttttttca t

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<210> 1967

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<400> 1967
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<210> 1968
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<400> 1968
tgcgcggcct ggcacgctg ctggccaaga acaaccggct cggcggggccc a 51

<210> 1969
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ctgtagccta agcaacagag caagatgccg tctctgaaaa ggaaagaaaa c 51

<210> 1970
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<221> misc_feature
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<210> 1971
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<223> 1 of 2 allelic variants (1972 is other entry)

<221> misc_feature
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<400> 1971
ggtgcttaag acagcagact gctgctttgc tgggccaggc ctgggtttat t 51

<210> 1972
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<212> DNA
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<223> 2 of 2 allelic variants (1971 is other entry)

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<210> 1973
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<221> misc_feature
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<210> 1974
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<223> 2 of 2 allelic variants (1973 is other entry)

<221> misc_feature
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<210> 1975
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<221> misc_feature
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<400> 1975
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<210> 1976
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<212> DNA
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<223> 2 of 2 allelic variants (1975 is other entry)

<221> misc_feature
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<223> Accession number cg38350552

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<210> 1977
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<212> DNA
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<223> 1 of 2 allelic variants (1978 is other entry)

<221> misc_feature
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cgctgggtgg cgccatcgat aagtctcttg aagccgtcaa gatggctccc g 51

<210> 1978
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<221> misc_feature
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<223> Accession number cg38403226

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<210> 1979
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<221> misc_feature
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<400> 1979
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<210> 1980
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<400> 1980

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<210> 1981

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<210> 1982

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (1981 is other entry)

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<400> 1982

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<210> 1983

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<400> 1984
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<400> 1985
tcagtgcagg gaataatacc caaggcggtt ctcccctggt ggcggccaac c 51

<210> 1986
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tcagtgcagg gaataatacc caaggcggtt ctcccctggt ggcggccaac c 51

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<223> 1 of 2 allelic variants (1988 is other entry)

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caaccgagct gccgcggcca aagtctcggt gtacaccatc gcctttggta c

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<210> 1988

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caaccgagct gccgcggcca aagtcccggt gtacaccatc gcctttggta c

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<223> 2 of 2 allelic variants (1989 is other entry)

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ggatgccacc gtcgaccgac cggcctaccg tgttacgtgc tgttgacgga a

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<210> 1994

<211> 51

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<223> 2 of 2 allelic variants (1993 is other entry)

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ggatgccacc gtcgaccgac cggcccaccg tgttacgtgc tgttgacgga a

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<210> 1995

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<223> 1 of 2 allelic variants (1996 is other entry)

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<223> Accession number cg38403231

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aacggagaag ctcgaagtat caaagcgggtt ggattcgtcg gatggggctc g

51

<210> 1996

<211> 51

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<223> Accession number cg38403231

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51

<210> 1997

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<400> 1997
tggcaactgg atcgggtgtca ttgggatcga cgaacggaga agctcgaagt a 51

<210> 1998
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<223> 2 of 2 allelic variants (1997 is other entry)

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<400> 1998
tggcaactgg atcgggtgtca ttgggttcga cgaacggaga agctcgaagt a 51

<210> 1999
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<223> 1 of 2 allelic variants (2000 is other entry)

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<400> 1999
cggtatgcct ttgatgggtca gtcacattga cgggcgctgg aacgctcgtg c 51

<210> 2000
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<223> 2 of 2 allelic variants (1999 is other entry)

<221> misc_feature
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<400> 2000
cggtatgcct ttgatggtca gtcacgttga cgggcgctgg aacgctcgtg c 51

<210> 2001
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<212> DNA
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<220>
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<223> 1 of 2 allelic variants (2002 is other entry)

<221> misc_feature
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<223> Accession number cg38403266

<400> 2001
acattgacgg gcgctggaac gctcgtgctg cccgctgaca cccgcaccga c 51

<210> 2002
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2001 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38403266

<400> 2002
acattgacgg gcgctggaac gctcgcgctg cccgctgaca cccgcaccga c 51

<210> 2003
<211> 51
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<223> 1 of 2 allelic variants (2004 is other entry)

<221> misc_feature
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<400> 2003
acgggcgctg gaacgctcgt gctgcccgt gacacccgca cgcacgacgg g 51

<210> 2004
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<223> 2 of 2 allelic variants (2003 is other entry)

<221> misc_feature
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<400> 2004
acgggcgctg gaacgctcgt gctgctcgt gacacccgca ccgacgacgg g 51

<210> 2005
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<223> 1 of 2 allelic variants (2006 is other entry)

<221> misc_feature
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<223> Accession number cg38403271

<400> 2005
tcaacggccc agtcggaatt tcgaaggatg atcgaaactt gctgacgaac t 51

<210> 2006
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2005 is other entry)

<221> misc_feature
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<223> Accession number cg38403271

<400> 2006
tcaacggccc agtcggaatt tcgaacgatg atcgaaactt gctgacgaac t 51

<210> 2007
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<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2008 is other entry)

<221> misc_feature
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<223> Accession number cg38403271

<400> 2007
atcgaaactt gctgacgaac tctcccatgg ttctgatgcc gggttcaagt a 51

<210> 2008
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (2007 is other entry)

<221> misc_feature
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<223> Accession number cg38403271

<400> 2008
atcgaaactt gctgacgaac tctccgatgg ttctgatgcc gggttcaagt a 51

<210> 2009
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2010 is other entry)

<221> misc_feature
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<400> 2009
agcagatcgc cgcacatgat ccggagcatt ccaagcggtt gttctccttt g 51

<210> 2010
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<212> DNA
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<220>
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<223> 2 of 2 allelic variants (2009 is other entry)

<221> misc_feature

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agcagatcgc cgcacatgat ccggaacatt ccaagcggtt gttctccttt g 51

<210> 2011
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<223> 1 of 2 allelic variants (2012 is other entry)

<221> misc_feature
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attccaagcg gttgttctcc ttgccaacc agatcgctgg tatggccagc c 51

<210> 2012
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<223> 2 of 2 allelic variants (2011 is other entry)

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<400> 2012
attccaagcg gttgttctcc ttgctaacc agatcgctgg tatggccagc c 51

<210> 2013
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<221> misc_feature
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<400> 2013
ctctcagatc ctcgacattc tgtctgcggg cctgattttc gtcgcgctgc t 51

<210> 2014
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<223> 2 of 2 allelic variants (2013 is other entry)

<221> misc_feature
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<400> 2014
ctctcagatc ctcgacattc tgtctacggg cctgattttc gtcgcgctgc t 51

<210> 2015
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<221> misc_feature
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<400> 2015
tggaagactc gccgagaaac tcgggttggc ctctgcgagc ccgcgtggag t 51

<210> 2016
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<400> 2016
tggaagactc gccgagaaac tcgggttggc ctctgcgagc ccgcgtggag t 51

<210> 2017
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<212> DNA
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<223> 1 of 2 allelic variants (2018 is other entry)

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<400> 2017
agaaactcgg gttggcctct gcgagcccg gcgtggagtgat gttcgcgggg t 51

<210> 2018
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<223> 2 of 2 allelic variants (2017 is other entry)

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<400> 2018
agaaactcgg gttggcctct gcgagtcgc gcgtggagtgat gttcgcgggg t 51

<210> 2019
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<213> Homo sapiens

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<223> 1 of 2 allelic variants (2020 is other entry)

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<400> 2019
ctgcgagccc gcgtggagtgc atgttcgcgg ggtcacctgc ttggactatc g 51

<210> 2020
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (2019 is other entry)

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<223> Accession number cg38403276

<400> 2020

ctgcgagccc gcgtggagtg atgtttgcgg ggtcacctgc ttggactatc g

51

<210> 2021

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2022 is other entry)

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51

<210> 2022

<211> 51

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<223> 2 of 2 allelic variants (2021 is other entry)

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<212> DNA

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<223> 1 of 2 allelic variants (2024 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38403276

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51

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<223> 2 of 2 allelic variants (2023 is other entry)

<221> misc_feature
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<223> Accession number cg38403276

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<210> 2025
<211> 51
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<223> 1 of 2 allelic variants (2026 is other entry)

<221> misc_feature
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<223> Accession number cg38403276

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<210> 2026
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<220>
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<221> misc_feature
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<210> 2027
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aggctgcgga ctttctatct gaatacgcca ccgaagatat ggaccttgcc g 51

<210> 2028
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<223> 2 of 2 allelic variants (2027 is other entry)

<221> misc_feature
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<400> 2028
aggctgcgga ctttctatct gaatatgcca ccgaagatat ggaccttgcc g 51

<210> 2029
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<223> 1 of 2 allelic variants (2030 is other entry)

<221> misc_feature
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<400> 2029
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<210> 2030
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2029 is other entry)

<221> misc_feature
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<400> 2030
gtgttgacgt gtaacttgga ttctctggct aagtcggcaa tcgtcactgg t 51

<210> 2031
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2032 is other entry)

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<400> 2031
aacttgatt ctccggctaa gtcggcaatc gtcactggtc ccgcgtggag c 51

<210> 2032
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2031 is other entry)

<221> misc_feature
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<223> Accession number cg38403345

<400> 2032
aacttgatt ctccggctaa gtcggtaatc gtcactggtc ccgcgtggag c 51

<210> 2033
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<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2034 is other entry)

<221> misc_feature
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<223> Accession number cg38403345

<400> 2033
actggtcccg cgtggagcga tacttctttg aggactgact gctgggcagg g 51

<210> 2034
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2033 is other entry)

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<400> 2034
actggtccccg cgtggagcga tacttttttg aggactgact gctgggcagg g 51

<210> 2035
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<212> DNA
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<223> 1 of 2 allelic variants (2036 is other entry)

<221> misc_feature
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<400> 2035
actgctgggc aggggtgagc gatgcgatga tggtgagaat ttcgcctatt c 51

<210> 2036
<211> 51
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2035 is other entry)

<221> misc_feature
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<400> 2036
actgctgggc aggggtgagc gatgcaatga tggtgagaat ttcgcctatt c 51

<210> 2037
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<212> DNA
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<223> 1 of 2 allelic variants (2038 is other entry)

<221> misc_feature

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<223> Accession number cg38403345

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51

<210> 2038

<211> 51

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<223> 2 of 2 allelic variants (2037 is other entry)

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<223> Accession number cg38403345

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ctgggcaggg gtgagc gatg cgatgggtgt gagaatttcg cctattcctt g

51

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<211> 51

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<223> 1 of 2 allelic variants (2040 is other entry)

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<223> Accession number cg38403345

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<210> 2040

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2039 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38403345

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cccgtcdata tcaccatccg tagtgtcgcg acgaagatcc cagatggccg t 51

<210> 2041
<211> 51
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<223> 1 of 2 allelic variants (2042 is other entry)

<221> misc_feature
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<223> Accession number cg38403345

<400> 2041
catatcacca tccgtagtgc cgcgacgaag atcccagatg gccgttcttg g 51

<210> 2042
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2041 is other entry)

<221> misc_feature
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<400> 2042
catatcacca tccgtagtgc cgcgatgaag atcccagatg gccgttcttg g 51

<210> 2043
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<212> DNA
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<223> 1 of 2 allelic variants (2044 is other entry)

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<400> 2043
tcttgacct gtatatgacg tatggtcttg tcgggtagct tactggcgca g 51

<210> 2044
<211> 51
<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (2043 is other entry)

<221> misc_feature

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<210> 2045

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<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2046 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38403345

<400> 2045

ccccagtatg gacggccccg gcctgttgct gggagtttct cgcgttccac c

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<210> 2046

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<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (2045 is other entry)

<221> misc_feature

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<223> Accession number cg38403345

<400> 2046

ccccagtatg gacggccccg gcctgctgct gggagtttct cgcgttccac c

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<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2048 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38403345

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gctgggagtt tctcgcgttc caccagcccc aaggacacca gcacgttgag g 51

<210> 2048
<211> 51
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<213> Homo sapiens

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<223> 2 of 2 allelic variants (2047 is other entry)

<221> misc_feature
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gctgggagtt tctcgcgttc caccaacccc aaggacacca gcacgttgag g 51

<210> 2049
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<212> DNA
<213> Homo sapiens

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<400> 2049
gttccaccag ccccaaggac accagcacgt tgaggggctc ccgaatcgtg t 51

<210> 2050
<211> 51
<212> DNA
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<221> misc_feature
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<400> 2050

gttcaccag cccaaggac accagtacgt tgaggggctc ccgaatcgtg t 51

<210> 2051
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<212> DNA
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<220>
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<223> 1 of 2 allelic variants (2052 is other entry)

<221> misc_feature
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<223> Accession number cg38403377

<400> 2051
aaatcttctt gacgatgacg tgcccttgtc tgagcgatcc ctgcttcgtc g 51

<210> 2052
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2051 is other entry)

<221> misc_feature
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<223> Accession number cg38403377

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<210> 2053
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<223> 1 of 2 allelic variants (2054 is other entry)

<221> misc_feature
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<223> Accession number cg38403377

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aatcttcttg acgatgacgt gcccttgctt gagcgatccc tgcttcgctg t 51

<210> 2054
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<212> DNA
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<223> 2 of 2 allelic variants (2053 is other entry)

<221> misc_feature
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<400> 2054
aatcttcttg acgatgacgt gccctggtct gagcgatccc tgcttcgtcg t 51

<210> 2055
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<223> 1 of 2 allelic variants (2056 is other entry)

<221> misc_feature
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<400> 2055
agcgatccct gcttcgtcgt tgcgtgccgt gagcgatccg gacgttgacac c 51

<210> 2056
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2055 is other entry)

<221> misc_feature
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<400> 2056
agcgatccct gcttcgtcgt tgcgtaccgt gagcgatccg gacgttgacac c 51

<210> 2057
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<212> DNA
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<220>
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<223> 1 of 2 allelic variants (2058 is other entry)

<221> misc_feature
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<400> 2057
cctctgcgac atatcgctgg gccgatgagg catcgacgat ctccccgcgg t 51

<210> 2058
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (2057 is other entry)

<221> misc_feature
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<223> Accession number cg38403377

<400> 2058
cctctgcgac atatcgctgg gccgacgagg catcgacgat ctccccgcgg t 51

<210> 2059
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2060 is other entry)

<221> misc_feature
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<223> Accession number cg38420254

<400> 2059
tccaggaaag gacaatgtcc tgcgagaaaa tcaggaggcc tccacttcct g 51

<210> 2060
<211> 50
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2059 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg38420254

<400> 2060

tccaggaaag gacaatgtcc tgcgaaaaat caggaggcct ccacttcctg

50

<210> 2061

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2062 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38420254

<400> 2061

cagtcaataa ttgtctttgt ggatgtgata attttggaga tacacttctg g

51

<210> 2062

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (2061 is other entry)

<221> misc_feature

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<223> Accession number cg38420254

<400> 2062

cagtcaataa ttgtctttgt ggatgagata attttggaga tacacttctg g

51

<210> 2063

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2064 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38421034

<400> 2063

ggtgactctg agcaagttct ggagccgcac gcacaagggg ctctgaaca g

51

<210> 2064

<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2063 is other entry)

<221> misc_feature
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<223> Accession number cg38421034

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ggtgactctg agcaagttct ggagctgcac gcacaagggg ctctgaaca g 51

<210> 2065
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (2066 is other entry)

<221> misc_feature
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<223> Accession number cg38421040

<400> 2065
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<210> 2066
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2065 is other entry)

<221> misc_feature
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<223> Accession number cg38421040

<400> 2066
ttggcccgtg tggtcaccct gtgtttattct ctctcccagc catggcctct c 51

<210> 2067
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2068 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38433776

<400> 2067
aggcgtcgta gtgggccacg atgacgatgg tgggaaggtc ctctccgcc a 51

<210> 2068
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2067 is other entry)

<221> misc_feature
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<223> Accession number cg38433776

<400> 2068
aggcgtcgta gtgggccacg atgacaatgg tgggaaggtc ctctccgcc a 51

<210> 2069
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> 1 of 2 allelic variants (2070 is other entry)

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<222> (0)...(0)
<223> Accession number cg38438371

<400> 2069
acctcgctga ttcgtgcaga ttgagctcag tgtgtctggg actgagctaa a 51

<210> 2070
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> 2 of 2 allelic variants (2069 is other entry)

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<222> (0)...(0)
<223> Accession number cg38438371

<400> 2070
acctcgctga ttcgtgcaga ttgagttcag tgtgtctggg actgagctaa a 51

<210> 2071
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2072 is other entry)

<221> misc_feature
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<223> Accession number cg38438371

<400> 2071
ctgggactga gctaaacagt gagacgtttg gaccgtcttt gatgtacaga g 51

<210> 2072
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<400> 2072
ctgggactga gctaaacagt gagacatttg gaccgtcttt gatgtacaga g 51

<210> 2073
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<212> DNA
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<223> 1 of 2 allelic variants (2074 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg38438475

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ggaagagggg aaggaaaagg cagcctaagg gaaggcgctg gcctgaatca

50

<210> 2074

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (0)...(0)

<223> Accession number cg38438475

<400> 2074

ggaagagggg aaggaaaagg cagccgtaag ggaaggcgct ggctgaatc a

51

<210> 2075

<211> 51

<212> DNA

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2076 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38438944

<400> 2075

acgcacactt accttgcagc ttcattgtcag agagcagctg agcagccagc a

51

<210> 2076

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2075 is other entry)

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<222> (0)...(0)

<223> Accession number cg38438944

<400> 2076

acgcacactt accttgcagc ttcattgtcag agagcagctg agcagccagc a

51

<210> 2077

<211> 51

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<220>
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<223> 1 of 2 allelic variants (2078 is other entry)

<221> misc_feature
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<223> Accession number cg38439545

<400> 2077
cctggcggcc agtaccagag cacagtccgg agtcttccgg cgggatgcat g 51

<210> 2078
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<220>
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<223> 2 of 2 allelic variants (2077 is other entry)

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<223> Accession number cg38439545

<400> 2078
cctggcggcc agtaccagag cacagcccgg agtcttccgg cgggatgcat g 51

<210> 2079
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<220>
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<223> 1 of 2 allelic variants (2080 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38444370

<400> 2079
gcatcgtttc gacgatgaac cccatcctgg gagcagatat gacgacgtac c 51

<210> 2080
<211> 51
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<220>
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<223> 2 of 2 allelic variants (2079 is other entry)

<221> misc_feature
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<223> Accession number cg38444370

<400> 2080
gcatcgtttc gacgatgaac cccattctgg gagcagatat gacgacgtac c 51

<210> 2081
<211> 51
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<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2082 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38444370

<400> 2081
agttcacctg ggaccaggtc gaccttgcta ctgtcgcaga caccggtcgg g 51

<210> 2082
<211> 51
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<220>
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<223> 2 of 2 allelic variants (2081 is other entry)

<221> misc_feature
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<223> Accession number cg38444370

<400> 2082
agttcacctg ggaccaggtc gacctcgcta ctgtcgcaga caccggtcgg g 51

<210> 2083
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (2084 is other entry)

<221> misc_feature
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<223> Accession number cg38446357

<400> 2083
tcgaggactt cgttttatcg gaggattcgt cgcgcaaccg atcaatctca g 51

<210> 2084
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2083 is other entry)

<221> misc_feature
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<223> Accession number cg38446357

<400> 2084
tcgaggactt cgttttatcg gaggactcgt cgcgcaaccg atcaatctca g 51

<210> 2085
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2086 is other entry)

<221> misc_feature
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<400> 2085
caatctcagt agcgaagtcc tcgatggtgt tgtagttcaa gttaaagctg g 51

<210> 2086
<211> 51
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<223> 2 of 2 allelic variants (2085 is other entry)

<221> misc_feature
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caatctcagt agcgaagtcc tcgatagtgt tgtagttcaa gttaaagctg g 51

<210> 2087
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (2088 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38446357

<400> 2087
tagcgaagtc ctcgatggtg ttgtagttca agtaaagcgt ggcaaacctc a 51

<210> 2088
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2087 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38446357

<400> 2088
tagcgaagtc ctcgatggtg ttgtacttca agtaaagcgt ggcaaacctc a 51

<210> 2089
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2090 is other entry)

<221> misc_feature
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<223> Accession number cg38446357

<400> 2089
ctggcaaacc tcaggtaagc gatggaatca agttcacgca gtggcccca g 51

<210> 2090
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (2089 is other entry)

<221> misc_feature

<222> (0)...(0)
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<400> 2090
ctggcaaacc tcaggtaagc gatgggatca agttcacgca gtggcccaa g 51

<210> 2091
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2092 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38446357

<400> 2091
acctcaggta agcgatggaa tcaagttcac gcagtggccc caagatcgcc a 51

<210> 2092
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (2091 is other entry)

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<222> (0)...(0)
<223> Accession number cg38446357

<400> 2092
acctcaggta agcgatggaa tcaagctcac gcagtggccc caagatcgcc a 51

<210> 2093
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (2094 is other entry)

<221> misc_feature
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<223> Accession number cg38446612

<400> 2093
gcgtagagt cgtcttgccg gcgccgttgc gaccactag accgaccttg t 51

<210> 2094
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2093 is other entry)

<221> misc_feature
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<223> Accession number cg38446612

<400> 2094
gcgttagagt cgtcttgccg gcgccattgc gaccactag accgaccttg t 51

<210> 2095
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<212> DNA
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<220>
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<223> 1 of 2 allelic variants (2096 is other entry)

<221> misc_feature
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<223> Accession number cg38446612

<400> 2095
gcgccgttgc gaccactag accgaccttg tccccagtag ctacctggaa a 51

<210> 2096
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (2095 is other entry)

<221> misc_feature
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<223> Accession number cg38446612

<400> 2096
gcgccgttgc gaccactag accgatcttg tccccagtag ctacctggaa a 51

<210> 2097
<211> 51
<212> DNA
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<220>

<221> misc_feature
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<223> 1 of 2 allelic variants (2098 is other entry)

<221> misc_feature
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<223> Accession number cg38446612

<400> 2097
tgcgaccac tagaccgacc ttgtcccag tagctacctg gaaactcacc g 51

<210> 2098
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2097 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38446612

<400> 2098
tgcgaccac tagaccgacc ttgtctccag tagctacctg gaaactcacc g 51

<210> 2099
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2100 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38446677

<400> 2099
gatcggcgt tcccgggttcg atagggggcg ttatagtcac gatcaccacc t 51

<210> 2100
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2099 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg38446677

<400> 2100

gatcggcggg tcccgggttcg ataggtggcg ttatagtcac gatcaccacc t

51

<210> 2101

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2102 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38446677

<400> 2101

atcatgggtg acgacgacga ggggtggtcc cgcgccgggc gtcgccgaaa g

51

<210> 2102

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2101 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38446677

<400> 2102

atcatgggtg acgacgacga ggggtggtccc cgcgccgggc tcgccgaaag

50

<210> 2103

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2104 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38453366

<400> 2103
tcttcgagtt tttgttcaag tctgggtctt ctgactgatt ttccaatgtc c 51

<210> 2104
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2103 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38453366

<400> 2104
tcttcgagtt tttgttcaag tctgggtctt ctgactgatt ttccaatgtc c 51

<210> 2105
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2106 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38453366

<400> 2105
ctgggtcttc tgactgattt tccaatgtcc aaggtgctga accgaatgca a 51

<210> 2106
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2105 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38453366

<400> 2106
ctgggtcttc tgactgattt tccaaagtcc aaggtgctga accgaatgca a 51

<210> 2107
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2108 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38453366

<400> 2107

tctgactgat tttccaatgt ccaaggtgct gaaccgaatg caatcaccat t

51

<210> 2108

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2107 is other entry)

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<223> Accession number cg38453366

<400> 2108

tctgactgat tttccaatgt ccaagttgct gaaccgaatg caatcaccat t

51

<210> 2109

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2110 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38453366

<400> 2109

ctgattttcc aatgtccaag gtgctgaacc gaatgcaatc accattcaat g

51

<210> 2110

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2109 is other entry)

<221> misc_feature
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<223> Accession number cg38453366

<400> 2110
ctgattttcc aatgtccaag gtgcttaacc gaatgcaatc accattcaat g

51

<210> 2111
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2112 is other entry)

<221> misc_feature
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<223> Accession number cg38453366

<400> 2111
ttttccaatg tccaaggtgc tgaaccgaat gcaatcacca ttcaatgaca g

51

<210> 2112
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2111 is other entry)

<221> misc_feature
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<223> Accession number cg38453366

<400> 2112
ttttccaatg tccaaggtgc tgaactgaat gcaatcacca ttcaatgaca g

51

<210> 2113
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2114 is other entry)

<221> misc_feature
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<223> Accession number cg38453366

<400> 2113

aatgtccaag gtgctgaacc gaatgcaatc accattcaat gacagctcaa c 51

<210> 2114

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2113 is other entry)

<221> misc_feature

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<223> Accession number cg38453366

<400> 2114

aatgtccaag gtgctgaacc gaatgtaatc accattcaat gacagctcaa c 51

<210> 2115

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2116 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38453366

<400> 2115

ctgaaccgaa tgcaatcacc attcaatgac agtcaactt ccaaatttct t 51

<210> 2116

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2115 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38453366

<400> 2116

ctgaaccgaa tgcaatcacc attcactgac agtcaactt ccaaatttct t 51

<210> 2117

<211> 50

<212> DNA

<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2118 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38453366

<400> 2117
accgaatgca atcaccattc aatgacagct caacttccaa atttctttga 50

<210> 2118
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2117 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38453366

<400> 2118
accgaatgca atcaccattc aatgaacagc tcaacttcca aatttctttg a 51

<210> 2119
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2120 is other entry)

<221> misc_feature
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<223> Accession number cg38453366

<400> 2119
caatcaccat tcaatgacag ctcaacttcc aaatttcttt gaatttcttt t 51

<210> 2120
<211> 51
<212> DNA
<213> Homo, sapiens

<220>

<221> misc_feature
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<223> 2 of 2 allelic variants (2119 is other entry)

<221> misc_feature
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<223> Accession number cg38453366

<400> 2120
caatcacat tcaatgacag ctcaatttcc aaatttcttt gaatttcttt t 51

<210> 2121
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2122 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38453366

<400> 2121
aatttctttt aacagaacaa tccaatatga aaatcagaat ctcttctgac g 51

<210> 2122
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2121 is other entry)

<221> misc_feature
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<223> Accession number cg38453366

<400> 2122
aatttctttt aacagaacaa tccaacatga aaatcagaat ctcttctgac g 51

<210> 2123
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2124 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg38453366

<400> 2123

ttaacagaac aatccaatat gaaaatcaga atctcttctg acggtgggag a

51

<210> 2124

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2123 is other entry)

<221> misc_feature

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<223> Accession number cg38453366

<400> 2124

ttaacagaac aatccaatat gaaaaccaga atctcttctg acggtgggag a

51

<210> 2125

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2126 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38606941

<400> 2125

tacagatata tacaagattc ccacctgtat gcaattctct gggtcattctg t

51

<210> 2126

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2125 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38606941

<400> 2126

tacagatata tacaagattc ccaccgtat gcaattctct gggtcattctg t

51

<210> 2127

<211> 41
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (16)...(0)
<223> 1 of 2 allelic variants (2128 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38624864

<400> 2127
accggtccca gacagtggga tgccaggacc ccttttgcag g

41

<210> 2128
<211> 41
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (16)...(0)
<223> 2 of 2 allelic variants (2127 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38624864

<400> 2128
accggtccca gacaggggga tgccaggacc ccttttgcag g

41

<210> 2129
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2130 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38628815

<400> 2129
gttgacagg ctctccaact cccagcctcc aggaatcctc cagcctcagc c

51

<210> 2130
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 2 of 2 allelic variants (2129 is other entry)

<221> misc_feature
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<223> Accession number cg38628815

<400> 2130
gttgacacagg ctctccaact ccagtcctcc aggaatcctc cagcctcagc c 51

<210> 2131
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2132 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38683973

<400> 2131
ctttcaaagt ctttaataac agggacgagc aaaataaatt agataaagcc'c 51

<210> 2132
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2131 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38683973

<400> 2132
ctttcaaagt ctttaataac agggatgagc aaaataaatt agataaagcc c 51

<210> 2133
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2134 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38683973

<400> 2133
agagatcgtg ctaaatacca gcttccagca gtggctatct gtcagtctag c 51

<210> 2134
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2133 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38683973

<400> 2134
agagatcgtg ctaaatacca gcttctagca gtggctatct gtcagtctag c 51

<210> 2135
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2136 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38691768

<400> 2135
ctcccaaagt gctgggatta caggcatgag ccaactgcgcc cagcctcaaa c 51

<210> 2136
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2135 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38691768

<400> 2136
ctcccaaagt gctgggatta caggcgtgag ccaactgcgcc cagcctcaaa c 51

<210> 2137
<211> 51

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2138 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38753049

<400> 2137
gcagccttga cctcctgggc tcaagcgatc cttctgcctc agcctcccaa g 51

<210> 2138
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2137 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38753049

<400> 2138
gcagccttga cctcctgggc tcaagtgatc cttctgcctc agcctcccaa g 51

<210> 2139
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2140 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38863525

<400> 2139
gggatcacca agatggaaga gtcggcagag tacgaggcag cgcggcataa a 51

<210> 2140
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 2 of 2 allelic variants (2139 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38863525

<400> 2140

gggatcacca agatggaaga gtcggtagag tacgaggcag cgcggcataa a

51

<210> 2141

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2142 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38864699

<400> 2141

gctgccgagc ctgggtctga gcaggcgggg atgaggacca ggtgctgagg c

51

<210> 2142

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2141 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38864699

<400> 2142

gctgccgagc ctgggtctga gcagggtggg atgaggacca ggtgctgagg c

51

<210> 2143

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2144 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38866989

<400> 2143
acagaaccat cctggcagat ggcaacggct gtagagaaga cccgcaggcc c 51

<210> 2144
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2143 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38866989

<400> 2144
acagaaccat cctggcagat ggcaatggct gtagagaaga cccgcaggcc c 51

<210> 2145
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2146 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38868761

<400> 2145
tctggggtag gggctgctcc cccaagtccc tgggggactg tctgggacat c 51

<210> 2146
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2145 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38868761

<400> 2146
tctggggtag gggctgctcc cccaaatccc tgggggactg tctgggacat c 51

<210> 2147
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2148 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38868761

<400> 2147

tctgggacat ccaggccctg tcttcttgct ttaaccactc acaacagaga a

51

<210> 2148

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2147 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38868761

<400> 2148

tctgggacat ccaggccctg tcttcgtgct ttaaccactc acaacagaga a

51

<210> 2149

<211> 45

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2150 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38868761

<400> 2149

aagaaggccc cacacttctc ccatccggcc tccacgtaaa cgcgt

45

<210> 2150

<211> 45

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2149 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38868761

<400> 2150
aagaaggccc cacacttctc ccatctggcc tccacgtaaa cgcgt 45

<210> 2151
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2152 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38879618

<400> 2151
gctgagagca ggagtagaag gtctgcaagc agcatttgag aagtcataga a 51

<210> 2152
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2151 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38879618

<400> 2152
gctgagagca ggagtagaag gtctgtaagc agcatttgag aagtcataga a 51

<210> 2153
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2154 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38879658

<400> 2153

gatcagaata actccagagc actgcggtgt ttctgactgg ctgaaattga t

51

<210> 2154

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2153 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38879658

<400> 2154

gatcagaata actccagagc actgctgtgt ttctgactgg ctgaaattga t

51

<210> 2155

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2156 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38880100

<400> 2155

tcagttacgc gattccgtga tcgcaaagct tgaaagactc gagcctggac g

51

<210> 2156

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2155 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38880100

<400> 2156

tcagttacgc gattccgtga tcgcagagct tgaaagactc gagcctggac g

51

<210> 2157

<211> 51

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2158 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38880100

<400> 2157
cgagcctgga cgccagggtga ttgtgagctc gttcaaccat gtgctgttat c 51

<210> 2158
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2157 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38880100

<400> 2158
cgagcctgga cgccagggtga ttgtgagctc gttcaaccat gtgctgttat c 51

<210> 2159
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2160 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38884905

<400> 2159
caaagcaact gtgaccgaaa accaactgca agattctcaa gagccctgaa g 51

<210> 2160
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2159 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38884905

<400> 2160
caaagcaact gtgaccgaaa accaaatgca agattctcaa gagccctgaa g 51

<210> 2161
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2162 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38884905

<400> 2161
aatcatccaa gaacacacta agcccgccaa gggcccaccc tgaccatgtg g 51

<210> 2162
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2161 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38884905

<400> 2162
aatcatccaa gaacacacta agccccaag ggcccaccct gaccatgtgg 50

<210> 2163
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2164 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg38890535

<400> 2163

cacacgcgtt ggcggagaaa cacttcgccc acagtgtagg gcctcgcttg g

51

<210> 2164

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2163 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38890535

<400> 2164

cacacgcgtt ggcggagaaa cactttgccc acagtgtagg gcctcgcttg g

51

<210> 2165

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2166 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38892055

<400> 2165

ccgagaggct ggcgaggggtg tgcagcacgg cgcagtgtgg caggggtccca g

51

<210> 2166

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2165 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38892055

<400> 2166

ccgagaggct ggcgaggggtg tgcagtacgg cgcagtgtgg caggggtccca g

51

<210> 2167

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2168 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38892055

<400> 2167
gatgaactgt cttcccacgg ccaccaggac gccactcgcc gcctgctgcc a

51

<210> 2168
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2167 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38892055

<400> 2168
gatgaactgt cttcccacgg ccaccgggac gccactcgcc gcctgctgcc a

51

<210> 2169
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2170 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38892771

<400> 2169
tctcttctgg tttcccaggc gtgtctgcct ctctgaaggt ttagctctcc c

51

<210> 2170
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 2 of 2 allelic variants (2169 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38892771

<400> 2170
tctcttctggtttcccaggcgtgtccgcctctctgaaggtttagctctcc c 51

<210> 2171
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2172 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38898718

<400> 2171
gacgaccgtgcccgtacaagccgaagcaac cgtcccaaaa agtacagaag g 51

<210> 2172
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2171 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38898718

<400> 2172
gacgaccgtgcccgtacaagccgaaacaac cgtcccaaaa agtacagaag g 51

<210> 2173
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2174 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38898718

<400> 2173
ccaggacgcc ctttcctcaa cccttctggc aagactccgg atgctggctc t 51

<210> 2174
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2173 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38898718

<400> 2174
ccaggacgcc ctttcctcaa cccttttggc aagactccgg atgctggctc t 51

<210> 2175
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2176 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38898718

<400> 2175
tttcctcaac ccttctggca agactccgga tgctggctct tcctcagtgg c 51

<210> 2176
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2175 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38898718

<400> 2176
tttcctcaac ccttctggca agactacgga tgctggctct tcctcagtgg c 51

<210> 2177
<211> 51

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2178 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38898718

<400> 2177
ccttctggca agactccgga tgctggctct tcctcagtgg cacgccctta a

51

<210> 2178
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2177 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38898718

<400> 2178
ccttctggca agactccgga tgctgactct tcctcagtgg cacgccctta a

51

<210> 2179
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2180 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38898734

<400> 2179
acatggtgtc accttgaata ggaatctcag gcaatcgaga cagagagagc c

51

<210> 2180
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 2 of 2 allelic variants (2179 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38898734

<400> 2180

acatggtgtc accttgaata ggaatttcag gcaatcgaga cagagagagc c

51

<210> 2181

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2182 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38899892

<400> 2181

gccaagatgc caacgagcag ggccaagatt tggggaagag ggaccaccat g

51

<210> 2182

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2181 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38899892

<400> 2182

gccaagatgc caacgagcag ggccaggatt tggggaagag ggaccaccat g

51

<210> 2183

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2184 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38902436

<400> 2183
tgaccgggcc tctgtggagg atgacagacg tagtggctgc cttcctagcc c 51

<210> 2184
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2183 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38902436

<400> 2184
tgaccgggcc tctgtggagg atgacggacg tagtggctgc cttcctagcc c 51

<210> 2185
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2186 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38907673

<400> 2185
gagcgacag agtgctgtcg ggggcatga atggccagaa tttcagagct g 51

<210> 2186
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2185 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg38907673

<400> 2186
gagcgacag agtgctgtcg ggggcatga atggccagaa tttcagagct g 51

<210> 2187
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2188 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38907673

<400> 2187

gagtagccgc aggtgcaagg acacagaaca gggtgaggaa agagtttggt t

51

<210> 2188

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2187 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg38907673

<400> 2188

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51

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51

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<223> 2 of 2 allelic variants (2189 is other entry)

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aagaaggggg tttgtttcag gaaagcactg ttagcatctt tgtttcaaag t 51

<210> 2192
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<210> 2193
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atctttgttt caaagttaac ctgtagacta agttcctccc aaagttagtt t

51

<210> 2194

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<400> 2194

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<210> 2195

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<222> (0)...(0)

<223> Accession number cg38916043

<400> 2195

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51

<210> 2196

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<223> Accession number cg38916043

<400> 2196

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51

<210> 2197

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<400> 2197
agcatggcgc cggagtgcgc tgcgatggtg atgaggtgac gcgggggggat t 51

<210> 2198
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<223> 2 of 2 allelic variants (2197 is other entry)

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<210> 2199
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<400> 2199
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<210> 2200
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<400> 2200
cgtgcatgg tgatgaggtg acgcgagggg attcccactc tccggttcgt g 51

<210> 2201
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<400> 2201
gcatggtga tgaggtgacg cggggggatt cccactctcc ggttcgtgct g 51

<210> 2202
<211> 51
<212> DNA
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<400> 2202
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<210> 2203
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<212> DNA
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<221> misc_feature
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<400> 2203
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<210> 2204

<211> 51

<212> DNA

<213> Homo sapiens

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aatggcgaat ggcgaaatgg tgctgcgcgg tggattatcc gttggtgtgc c

51

<210> 2205

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<223> 1 of 2 allelic variants (2206 is other entry)

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<223> Accession number cg38916043

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cacggcgtca tgcttgctca gctcaaccgc ggtgaaacag tcagaggatg g

51

<210> 2206

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2205 is other entry)

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<223> Accession number cg38916043

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51

<210> 2207

<211> 51

<212> DNA

<213> Homo sapiens

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<400> 2207
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<210> 2208
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<223> 2 of 2 allelic variants (2207 is other entry)

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<400> 2208
gcgtcatgct tgctcagctc aaccgtggtg aaacagtcag aggatggata t 51

<210> 2209
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<223> 1 of 2 allelic variants (2210 is other entry)

<221> misc_feature
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<400> 2209
acgatgaggg ccataccga gaagacaacg gccaccactc gcagaccacc t 51

<210> 2210
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<212> DNA
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<223> 2 of 2 allelic variants (2209 is other entry)

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acgatgaggg ccataccga gaagagaacg gccaccactc gcagaccacc t 51

<210> 2211
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gggaggatcg cggccactga ccacgccagt accggcaggg tcaggatcag c 51

<210> 2212
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<400> 2212
gggaggatcg cggccactga ccacgtcagt accggcaggg tcaggatcag c 51

<210> 2213
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<223> 1 of 2 allelic variants (2214 is other entry)

<221> misc_feature
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<223> Accession number cg38922874

<400> 2213
taccgggaca gttacgagtc catgtccgag ccgccattg ctcacctttt g 51

<210> 2214
<211> 51
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<223> 2 of 2 allelic variants (2213 is other entry)

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51

<210> 2215
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<223> 1 of 2 allelic variants (2216 is other entry)

<221> misc_feature
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<400> 2215
tctgccccaa gggcgagaag acgggcttcg cagcgaccct cgggggtcca t

51

<210> 2216
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<400> 2216
tctgccccaa gggcgagaag acgggttcgc agcgaccctc ggggggtccat

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<210> 2217
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<212> DNA
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<221> misc_feature
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<223> Accession number cg38925867

<400> 2217
cgaggcggtgta aggcctcacc gcgcagccca catcatcatc gtggagacga t

51

<210> 2218
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cgaggcggtgta aggcctcacc gcgcacccac atcatcatcg tggagacgat

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<210> 2219
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51

<210> 2220
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<400> 2220
atggcaagag ctggccaccc accctcccc ttccttccca aaggctgtgt 50

<210> 2221
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<400> 2221
gagctggcca cccaccccct ccccttcctt ccaaaggct gtgttttgtc t 51

<210> 2222
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<400> 2222
gagctggcca cccaccccct cccctccttc ccaaaggctg tggtttgtct 50

<210> 2223
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<212> DNA
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<223> 1 of 2 allelic variants (2224 is other entry)

<221> misc_feature
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<223> Accession number cg39331132

<400> 2223
tgtgacatgc tgttttaatt tcagtgacct cttggaaggc actgtcccca a 51

<210> 2224
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<223> 2 of 2 allelic variants (2223 is other entry)

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<400> 2224
tgtgacatgc tgttttaatt tcagtaacct cttggaaggc actgtcccca a 51

<210> 2225
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<223> 1 of 2 allelic variants (2226 is other entry)

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<400> 2225
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<210> 2226
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<223> 2 of 2 allelic variants (2225 is other entry)

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<223> Accession number cg39357997

<400> 2226

cctctaggaa cccaaccttc tgcgtccata cacgcgctcg cgcgcacacg c

51

<210> 2227

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2228 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39357997

<400> 2227

gcacacacac acacacacac acacacagca agcaagccat ctccggtcac a

51

<210> 2228

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<212> DNA

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<223> 2 of 2 allelic variants (2227 is other entry)

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<223> Accession number cg39357997

<400> 2228

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<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2230 is other entry)

<221> misc_feature
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<400> 2229
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51

<210> 2230
<211> 51
<212> DNA
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<400> 2230
tgtttttttac accagcagtc aaaaacagtt acttttgata ttgcatgtgt c

51

<210> 2231
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (2232 is other entry)

<221> misc_feature
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<400> 2231
aaaggaatat cctctcacca gagacacgcg gcggccaggc agggccggag c

51

<210> 2232
<211> 50
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<221> misc_feature
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<221> misc_feature
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<223> Accession number cg39413590

<400> 2232

aaaggaatat cctctcacca gagaccgcgg cggccaggca gggccggagc

50

<210> 2233

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2234 is other entry)

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<223> Accession number cg39413590

<400> 2233

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51

<210> 2234

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2233 is other entry)

<221> misc_feature

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<223> Accession number cg39413590

<400> 2234

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51

<210> 2235

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<212> DNA

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<223> 1 of 2 allelic variants (2236 is other entry)

<221> misc_feature

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<223> Accession number cg39434475

<400> 2235

gcctgtgtt ggatggaatc cggaggaccc cagctccctg agcagccct c

51

<210> 2236

<211> 50
<212> DNA
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<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
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<400> 2236
gccctgctgt ggatggaatc cggagacccc agctccctga gcagcccctc

50

<210> 2237
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (2238 is other entry)

<221> misc_feature
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<223> Accession number cg39457156

<400> 2237
cagcgttaag tggcataccc ggaaggaaac acagcagctc ttggatatga t

51

<210> 2238
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (2237 is other entry)

<221> misc_feature
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<400> 2238
cagcgttaag tggcataccc ggaagaaaac acagcagctc ttggatatga t

51

<210> 2239
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<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2240 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39457156

<400> 2239

actatggtgc catggtcgtc gatgcagcgc tgttcctgcc acagtcacga c

51

<210> 2240

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2239 is other entry)

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<223> Accession number cg39457156

<400> 2240

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<210> 2241

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<212> DNA

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<223> Accession number cg39462273

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51

<210> 2242

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<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (2241 is other entry)

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<400> 2242
gaacggacgc tgcctcctag tattaaaata cccaactctt tgatatctcc c 51

<210> 2243
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<223> Accession number cg39466668

<400> 2243
atatacctta ttagcatttc ctttcaaaaa aacagttgtc tttggatttt 50

<210> 2244
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (2243 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39466668

<400> 2244
atatacctta ttagcatttc ctttcaaaaa aaacagttgt ctttggattt t 51

<210> 2245
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2246 is other entry)

<221> misc_feature

<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39466668

<400> 2245
ttattagcat ttcctttcaa aaaaacagtt gtctttggat tttgattgtc 50

<210> 2246
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2245 is other entry)

<221> misc_feature
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<223> Accession number cg39466668

<400> 2246
ttattagcat ttcctttcaa aaaaacagtt tgtctttgga ttttgattgt c 51

<210> 2247
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2248 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39485034

<400> 2247
gtaagaactt ggtaggcagg ttgcgctgcc acacattcgc gatgaacgcg t 51

<210> 2248
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2247 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39485034

<400> 2248
gtaagaactt ggtaggcagg ttgcgttgcc acacattcgc gatgaacgcg t 51

<210> 2249
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2250 is other entry)

<221> misc_feature
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<223> Accession number cg39507328

<400> 2249
cgaggagaga ctaacttttc actttgtttc acctgtgatc tgggtctggc g 51

<210> 2250
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (2249 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39507328

<400> 2250
cgaggagaga ctaacttttc actttatttc acctgtgatc tgggtctggc g 51

<210> 2251
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2252 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39507822

<400> 2251
tcagctttcc ttaagccctc ttccagaaca aatgagacac ttacatgttt c 51

<210> 2252
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2251 is other entry)

<221> misc_feature
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<223> Accession number cg39507822

<400> 2252
tcagctttcc ttaagccctc ttccataaca aatgagacac ttacatgttt c 51

<210> 2253
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2254 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39507822

<400> 2253
tcaaaattcc tagagtcaag atctgtttct tgactctggt gcaccgggag a 51

<210> 2254
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2253 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39507822

<400> 2254
tcaaaattcc tagagtcaag atctgtttct tgactctggt gcaccgggag a 51

<210> 2255
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2256 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39512670

<400> 2255

aattaagatc ctccattctt tctatgaaaa gtcagggaca aggcaagaca t

51

<210> 2256

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2255 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39512670

<400> 2256

aattaagatc ctccattctt tctataaaaa gtcagggaca aggcaagaca t

51

<210> 2257

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2258 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39515262

<400> 2257

cacttccac tgtgctctgc caagcctctg tggagaggag cctccacct g

51

<210> 2258

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2257 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39515262

<400> 2258
cacttccac tgtgctctgc caagcgtctg tggagaggag ccctccacct g 51

<210> 2259
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<212> DNA
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<223> 1 of 2 allelic variants (2260 is other entry)

<221> misc_feature
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<223> Accession number cg39515274

<400> 2259
gagccatggc cgagccctgc tggggccggc gcgggcgagg gcgggacgcg g 51

<210> 2260
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2259 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39515274

<400> 2260
gagccatggc cgagccctgc tggggcgcgc gcgggcgagg gcgggacgcg g 51

<210> 2261
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (2262 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39515274

<400> 2261
gctttccagc ggccgggagg agcgggtcct cggggccagg aaggtgagcg c 51

<210> 2262
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2261 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39515274

<400> 2262

gctttccagc ggccgggagg agcggatcct cggggccagg aaggtagagc c

51

<210> 2263

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2264 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39515274

<400> 2263

ggtgagcgca cctttcgctg agcacagggc ggcaccgcgc gggcggaccc c

51

<210> 2264

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2263 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39515274

<400> 2264

ggtgagcgca cctttcgctg agcacggggc ggcaccgcgc gggcggaccc c

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<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2266 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39515274

<400> 2265
ttcctctctt cgccctgccca accacttttt tagtttcttc tcctctctcg g 51

<210> 2266
<211> 50
<212> DNA
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2265 is other entry)

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<221> misc_feature
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<223> Accession number cg39515274

<400> 2266
ttcctctctt cgccctgccca accacttttt agtttcttct catctctcgg 50

<210> 2267
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2268 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39516519

<400> 2267
tagagcaggt acgcactgat ttgaagagta gttggtgtgt ctcccatact g 51

<210> 2268
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2267 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg39516519

<400> 2268
tagagcaggt acgcactgat ttgaaaagta gttggtgtgt ctcccatact g 51

<210> 2269
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2270 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39517070

<400> 2269
cagaaccagg acgattgctc cgaaggcccc accacgagga aggcagccag g 51

<210> 2270
<211> 50
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (2269 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg39517070

<400> 2270
cagaaccagg acgattgctc cgaagcccca ccacgaggaa ggcagccagg 50

<210> 2271
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2272 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39517771

<400> 2271
acggctctct cgacggacag gtcggggttt tcttcgtgat gatcgtggca g 51

<210> 2272
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2271 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39517771

<400> 2272
acggctctct cgacggacag gtcggagttt tcttcgtgat gatcgtggca g 51

<210> 2273
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2274 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39517771

<400> 2273
ttgtcggttt ggcgatcatc gtcactattt tccgttcccg tcgcaccact t 51

<210> 2274
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2273 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39517771

<400> 2274
ttgtcggttt ggcgatcatc gtcaccattt tccgttcccg tcgcaccact t 51

<210> 2275
<211> 51

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2276 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39517771

<400> 2275
aaccggcttg ttcaacgtgg cctggctcat gattgcggtg ccactggtgg t 51

<210> 2276
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2275 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39517771

<400> 2276
aaccggcttg ttcaacgtgg cctggctcat gattgcggtg ccactggtgg t 51

<210> 2277
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2278 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39521356

<400> 2277
cccagagcaa gctgcggctc attcacggac ccctcagaac aggctggatg a 51

<210> 2278
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 2 of 2 allelic variants (2277 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39521356

<400> 2278

cccagagcaa gctgcggctc attcatggac ccctcagaac aggctggatg a

51

<210> 2279

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2280 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39522018

<400> 2279

atactctgtg tgtctatgtg cttagcgggg aacctccaga ggaggtggtg a

51

<210> 2280

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2279 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39522018

<400> 2280

atactctgtg tgtctatgtg cttagtgggg aacctccaga ggaggtggtg a

51

<210> 2281

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2282 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39523840

<400> 2281
tggcattttt aagtcgtgta gaactcacia ctttttaaac accttcccat a 51

<210> 2282
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2281 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39523840

<400> 2282
tggcattttt aagtcgtgta gaacttacia ctttttaaac accttcccat a 51

<210> 2283
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2284 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39524105

<400> 2283
tcttgagacc aggcatagtg ctgggcactg gtgcaagcga agtggaagtc g 51

<210> 2284
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2283 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39524105

<400> 2284
tcttgagacc aggcatagtg ctgggtactg gtgcaagcga agtggaagtc g 51

<210> 2285
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2286 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39524138

<400> 2285

gctgacgaga tgatcgcccg cgacgggttc atctggcgca ggccttgagg a

51

<210> 2286

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2285 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39524138

<400> 2286

gctgacgaga tgatcgcccg cgacgagttc atctggcgca ggccttgagg a

51

<210> 2287

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2288 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39524138

<400> 2287

cgagatgatc gcccgcgacg gggtcatctg gcgcaggcct tgaggaggag a

51

<210> 2288

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2287 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39524138

<400> 2288
cgagatgatc gcccgcgacg gggtcgtctg ggcaggcct tgaggaggag a 51

<210> 2289
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2290 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39524138

<400> 2289
gatcgtcacg ctcaacgaca ccaccgctc gaagattggt ggggccatcg t 51

<210> 2290
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2289 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39524138

<400> 2290
gatcgtcacg ctcaacgaca ccaccctcg aagattggtg gggccatcgt 50

<210> 2291
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2292 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg39524138

<400> 2291
aggcccgctcg taccggttggg tctggatctg ggttggttca caccctcatt t 51

<210> 2292
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2291 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39524138

<400> 2292
aggcccgctcg taccggttggg tctgggtctg ggttggttca caccctcatt t 51

<210> 2293
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2294 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39524728

<400> 2293
agcccaccac cgccgggtac ctgcacagcc acatatatgc aagtacacac a 51

<210> 2294
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2293 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39524728

<400> 2294
agcccaccac cgccgggtac ctgcaaagcc acatatatgc aagtacacac a 51

<210> 2295
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2296 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39524728

<400> 2295
cacaggcact cgcacgcatg catgctcatg caacacacat gtacactcta c 51

<210> 2296
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2295 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39524728

<400> 2296
cacaggcact cgcacgcatg catgcccacat caacacacat gtacactcta c 51

<210> 2297
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2298 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39524728

<400> 2297
caccagccac acacaagtac tcatacgcat acatgcccac acacaaagta c 51

<210> 2298
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2297 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39524728

<400> 2298
caccagccac acacaagtac tcatatgcat acatgcccac acacaaagta c 51

<210> 2299
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2300 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39524728

<400> 2299
cccacacaca aagtacacac acgtacacca tatgcatatg tatgcactca t 51

<210> 2300
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2299 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39524728

<400> 2300
cccacacaca aagtacacac acgtaaacca tatgcatatg tatgcactca t 51

<210> 2301
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
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<223> Accession number cg39524728

<400> 2301

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51

<210> 2302

<211> 51

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<223> 2 of 2 allelic variants (2301 is other entry)

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<223> Accession number cg39524728

<400> 2302

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51

<210> 2303

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2304 is other entry)

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<223> Accession number cg39524728

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caagacacaa acacatgtac acgcacacat gcgcacacac acgtacatct a

51

<210> 2304

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2303 is other entry)

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<223> Accession number cg39524728

<400> 2304

caagacacaa acacatgtac acgcatacat gcgcacacac acgtacatct a

51

<210> 2305

<211> 51
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<223> 1 of 2 allelic variants (2306 is other entry)

<221> misc_feature
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<400> 2305
gcgcgcctac cttgccagac cctgggcacg cctgccttca ggtgccagg c

51

<210> 2306
<211> 50
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<223> Accession number cg39530012

<400> 2306
gcgcgcctac cttgccagac cctgggcacg ctgccttcag ggtgccaggc

50

<210> 2307
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (2308 is other entry)

<221> misc_feature
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<223> Accession number cg39530012

<400> 2307
gctacagcct gcagtcctga gcgtgaggtg ctatacttcc caggagacat c

51

<210> 2308
<211> 51
<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2307 is other entry)

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<223> Accession number cg39530012

<400> 2308

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<210> 2309

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2310 is other entry)

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<222> (0)...(0)

<223> Accession number cg39530051

<400> 2309

aaatttcatt actttttatg gctgagtaac atcccatcgt atggatggac t

51

<210> 2310

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2309 is other entry)

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<223> Accession number cg39530051

<400> 2310

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51

<210> 2311

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2312 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<400> 2311
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50

<210> 2312
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2311 is other entry)

<221> misc_feature
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<223> Accession number cg39535156

<400> 2312
gcgggtcgtg acgtagccgg gcagggcga accggtaccg ggaaaacgat g

51

<210> 2313
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2314 is other entry)

<221> misc_feature
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<400> 2313
ttgaagcagg gcagtaaatt taccagcttc ttgatgaaac ataactccag t

51

<210> 2314
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2313 is other entry)

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<400> 2314
ttgaagcagg gcagtaaatt taccaacttc ttgatgaaac ataactccag t 51

<210> 2315
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2316 is other entry)

<221> misc_feature
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<400> 2315
atactgctaa taaatgacag tggctgctaa catctcttga gcactgcct t 51

<210> 2316
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2315 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39535310

<400> 2316
atactgctaa taaatgacag tggctactaa catctcttga gcactgcct t 51

<210> 2317
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2318 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39535310

<400> 2317
gaaggacag gacttggctg ctgattccat gtggaggagc tgctcacggt g 51

<210> 2318

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39535310

<400> 2318

gaaggacag gacttgctg ctgatcccat gtggaggagc tgctcacggt g

51

<210> 2319

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2320 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39536028

<400> 2319

atcagtcaag ccgtcatgat catcgtggga aaagaagtaa ccaggcagaa t

51

<210> 2320

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2319 is other entry)

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<223> Accession number cg39536028

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51

<210> 2321

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature
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<223> Accession number cg39536028

<400> 2321
agcaggtagag ggtcactacc tctccttttc ctgcctgccc cggcctctcc c 51

<210> 2322
<211> 51
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<223> 2 of 2 allelic variants (2321 is other entry)

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<400> 2322
agcaggtagag ggtcactacc tctcattttc ctgcctgccc cggcctctcc c 51

<210> 2323
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<223> 1 of 2 allelic variants (2324 is other entry)

<221> misc_feature
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<223> Accession number cg39536028

<400> 2323
aaccatgggt ttagtgtcca ccagacttaa aggaccagg accttctcac c 51

<210> 2324
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (2323 is other entry)

<221> misc_feature
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<223> Accession number cg39536028

<400> 2324

aaccatgggt ttagtgcca ccagatttaa aggaccagg accttctcac c

51

<210> 2325

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2326 is other entry)

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<222> (0)...(0)

<223> Accession number cg39537504

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caggtctgtg aagcttctgg gctcaggaga gtcttgccg acgcttgctc g

51

<210> 2326

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2325 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39537504

<400> 2326

caggtctgtg aagcttctgg gctcaagaga gtcttgccg acgcttgctc g

51

<210> 2327

<211> 50

<212> DNA

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<221> misc_feature

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<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39537504

<400> 2327
tcgggaacct cgccatgccg cgcgcacctc cctaccccac cgccagtc 50

<210> 2328
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2327 is other entry)

<221> misc_feature
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<223> Accession number cg39537504

<400> 2328
tcgggaacct cgccatgccg cgcgcgacct ccctacccca ccgcagtc c 51

<210> 2329
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (2330 is other entry)

<221> misc_feature
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<223> Accession number cg39537504

<400> 2329
ccatgccgcc gccacctccc taccacccc gccagtcctt cgccggcgct c 51

<210> 2330
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<223> 2 of 2 allelic variants (2329 is other entry)

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<223> Accession number cg39537504

<400> 2330
ccatgccgcc gccacctccc tacctaccc gccagtcctt cgccggcgct c 51

<210> 2331
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<213> Homo sapiens

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<223> 1 of 2 allelic variants (2332 is other entry)

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51

<210> 2332

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<223> Accession number cg39537504

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51

<210> 2333

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<223> 1 of 2 allelic variants (2334 is other entry)

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<223> Accession number cg39540190

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tcagatccat gagagctgca aagttacgga agcgtgagcg ccgctggagg a

51

<210> 2334

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2333 is other entry)

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<223> Accession number cg39540190

<400> 2334
tcagatccat gagagctgca aagttgcgga agcgtgagcg ccgctggagg a 51

<210> 2335
<211> 51
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<223> 1 of 2 allelic variants (2336 is other entry)

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<223> Accession number cg39540317

<400> 2335
gaaagtcaag cagtgggaag tacatggagc tctcagccct gctcccatct g 51

<210> 2336
<211> 51
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<223> 2 of 2 allelic variants (2335 is other entry)

<221> misc_feature
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<400> 2336
gaaagtcaag cagtgggaag tacatagagc tctcagccct gctcccatct g 51

<210> 2337
<211> 51
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<223> 1 of 2 allelic variants (2338 is other entry)

<221> misc_feature
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<223> Accession number cg39540317

<400> 2337

tcagcagatg ggccactgac tgagcgctgc cccgtccctg gtgctactgg t

51

<210> 2338

<211> 51

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<400> 2338

tcagcagatg ggccactgac tgagcgctgc cccgtccctg gtgctactgg t

51

<210> 2339

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2340 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39540317

<400> 2339

tgggccactg actgagcgct gccccgtccc tgggtgctact ggtctttcta a

51

<210> 2340

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2339 is other entry)

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<223> Accession number cg39540317

<400> 2340

tgggccactg actgagcgct gccccatccc tgggtgctact ggtctttcta a

51

<210> 2341

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2342 is other entry)

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<223> Accession number cg39540317

<400> 2341
cccgtccctg gtgctactgg tcttttctaaa cttagcacc tggagagtcc a 51

<210> 2342
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<212> DNA
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<223> 2 of 2 allelic variants (2341 is other entry)

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<223> Accession number cg39540317

<400> 2342
cccgtccctg gtgctactgg tctttttctaaa cttagcacc tggagagtcc a 51

<210> 2343
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (2344 is other entry)

<221> misc_feature
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<400> 2343
ggtgctactg gtcttttctaa acttagcacc ctggagagtc caaggaggca g 51

<210> 2344
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2343 is other entry)

<221> misc_feature
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<400> 2344
ggtgctactg gtcttttctaa acttaacacc ctggagagtc caaggaggca g 51

<210> 2345
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2346 is other entry)

<221> misc_feature
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<223> Accession number cg39540409

<400> 2345
catgttttct tcttgagaa agtgtcagaa aagtgtacag cctggggcca a 51

<210> 2346
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2345 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39540409

<400> 2346
catgttttct tcttgagaa agtgtagaa aagtgtacag cctggggcca a 51

<210> 2347
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2348 is other entry)

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<222> (0)...(0)
<223> Accession number cg39540537

<400> 2347
actggcggca ggaatgaatc agcagatagt cattttcccg cagcccttct a 51

<210> 2348
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2347 is other entry)

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<223> Accession number cg39540537

<400> 2348
actggcggca ggaatgaatc agcaggtagt cattttcccg cagcccttct a

51

<210> 2349
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (2350 is other entry)

<221> misc_feature
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<223> Accession number cg39541853

<400> 2349
ctttcccat tagattttgt gtgtgctgt gtttattatt ttggtaggcg g

51

<210> 2350
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<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2349 is other entry)

<221> misc_feature
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<400> 2350
ctttcccat tagattttgt gtgtgtgtgt gtttattatt ttggtaggcg g

51

<210> 2351
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2352 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39543172

<400> 2351
cagcagccgg gagtagtgcc cgcttcccc acaggaagtt cctgtctgcg c 51

<210> 2352
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2351 is other entry)

<221> misc_feature
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<223> Accession number cg39543172

<400> 2352
cagcagccgg gagtagtgcc cgcttgcccc acaggaagtt cctgtctgcg c 51

<210> 2353
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2354 is other entry)

<221> misc_feature.
<222> (0)...(0)
<223> Accession number cg39543172

<400> 2353
agcagccggg agtagtgccc gcttccccca caggaagttc ctgtctgcgc c 51

<210> 2354
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2353 is other entry)

<221> misc_feature

<222> (0)...(0)
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<400> 2354
agcagccggg agtagtgccc gcttcgccc caggaagttc ctgtctgcgc c 51

<210> 2355
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2356 is other entry)

<221> misc_feature
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<400> 2355
ggaagttcct gtctgcgccc acccaggggt tgggtgtgag cagcttctca g 51

<210> 2356
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2355 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39543172

<400> 2356
ggaagttcct gtctgcgccc acccaggggt tgggtgtgag cagcttctca g 51

<210> 2357
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2358 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39543172

<400> 2357
agcaagcccc acagctgtcc tgcacgagtg gaggtgtctc acacagccct t 51

<210> 2358
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2357 is other entry)

<221> misc_feature
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<223> Accession number cg39543172

<400> 2358
agcaagcccc acagctgtcc tgcacaagtg gaggctgctc acacagccct t 51

<210> 2359
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (2360 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39545387

<400> 2359
gtagagaggg ccagtgtggt gcgattttgt gggaggagtt gagattggat g 51

<210> 2360
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2359 is other entry)

<221> misc_feature
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<223> Accession number cg39545387

<400> 2360
gtagagaggg ccagtgtggt gcgatcttgt gggaggagtt gagattggat g 51

<210> 2361
<211> 51
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<223> 1 of 2 allelic variants (2362 is other entry)

<221> misc_feature
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<223> Accession number cg39545387

<400> 2361
gtagaggagg aagtgactgt cggcaagtgt ggagagagga gccccagctt c 51

<210> 2362
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2361 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39545387

<400> 2362
gtagaggagg aagtgactgt cggcatgtgt ggagagagga gccccagctt c 51

<210> 2363
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2364 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39545387

<400> 2363
cttcacctta atgtgaggct gattcgtgaa cccatttatt cttgtggcag a 51

<210> 2364
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2363 is other entry)

<221> misc_feature
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<223> Accession number cg39545387

<400> 2364

cttcacctta atgtgaggct gattcatgaa cccatttatt cttgtggcag a

51

<210> 2365

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2366 is other entry)

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<223> Accession number cg39545619

<400> 2365

gaggggccga cgagctgggt ctgcgcaaag cagtgaaggc cgagtttggc g

51

<210> 2366

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2365 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39545619

<400> 2366

gaggggccga cgagctgggt ctgcgtaaag cagtgaaggc cgagtttggc g

51

<210> 2367

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2368 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39545619

<400> 2367

gccgacgagc tgggtctgcg caaagcagtg aaggccgagt ttggcggggg c

51

<210> 2368

<211> 51
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<223> 2 of 2 allelic variants (2367 is other entry)

<221> misc_feature
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<223> Accession number cg39545619

<400> 2368
gccgacgagc tgggtctgcg caaagtagtg aaggccgagt ttggcggggg c 51

<210> 2369
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2370 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39545619

<400> 2369
agtgaaggcc gagtttggcg ggggcacccg cggcttctcc tgcgaggagg a 51

<210> 2370
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2369 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39545619

<400> 2370
agtgaaggcc gagtttggcg ggggcgcccg cggcttctcc tgcgaggagg a 51

<210> 2371
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 1 of 2 allelic variants (2372 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39545619

<400> 2371
gctgcagaat ttgcgtgccca agcagggaga agcactccac aacgtgcgct t 51

<210> 2372
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2371 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39545619

<400> 2372
gctgcagaat ttgcgtgccca agcagagaga agcactccac aacgtgcgct t 51

<210> 2373
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2374 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39545648

<400> 2373
ctagagtata attaaggaga ctgcctgtgc ttgctgctgg aggggtgatg t 51

<210> 2374
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2373 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39545648

<400> 2374
ctagagtata attaaggaga ctgcccgctgc ttgctgctgg aggggtgatg t 51

<210> 2375
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2376 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26.

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39559225

<400> 2375
tccagcttta aaaaaaacac acacaaaact ttgccacagt gttgcatgag 50

<210> 2376
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2375 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39559225

<400> 2376
tccagcttta aaaaaaacac acacacaaac ttgccacag tgttgcatga g 51

<210> 2377
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2378 is other entry)

<221> misc_feature
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<223> Accession number cg39559225

<400> 2377

aaaactttgc cacagtgttg catgagaata tgcttgcttt catgtgctgg c

51

<210> 2378

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2377 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39559225

<400> 2378

aaaactttgc cacagtgttg catgaaaata tgcttgcttt catgtgctgg c

51

<210> 2379

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2380 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39559767

<400> 2379

gcaaaccggg catggagacc ccatctcagg tctgtgcttc tctgggggcc a

51

<210> 2380

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2379 is other entry)

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<222> (0)...(0)

<223> Accession number cg39559767

<400> 2380

gcaaaccggg catggagacc ccatcccagg tctgtgcttc tctgggggcc a

51

<210> 2381

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2382 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39560753

<400> 2381
tcggctgtct tctgctgccg gcaggaacgg ggctcaacc ttctctgggc a 51

<210> 2382
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2381 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39560753

<400> 2382
tcggctgtct tctgctgccg gcaggtacgg ggctcaacc ttctctgggc a 51

<210> 2383
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2384 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39564627

<400> 2383
gaggagccca gaacactggg ggctgtgcta ctagcaccat agaattcagg t 51

<210> 2384
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2383 is other entry)

<221> misc_feature
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<221> misc_feature
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<223> Accession number cg39564627

<400> 2384
gaggagccca gaacactggg ggctggctac tagcaccata gaattcaggt 50

<210> 2385
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (2386 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39564627

<400> 2385
cataacaagg cgtaggggtat ggggtgacat ttctacattg cagcagcaca t 51

<210> 2386
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2385 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39564627

<400> 2386
cataacaagg cgtaggggtat ggggtaacat ttctacattg cagcagcaca t 51

<210> 2387
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2388 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg39564709

<400> 2387

gttggtcagt ggggggtgggc ctgggcctaa cttttcaagc tgaagatgct c

51

<210> 2388

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2387 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39564709

<400> 2388

gttggtcagt ggggggtgggc ctgggcctaac ttttcaagct gaagatgctc

50

<210> 2389

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2390 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39565239

<400> 2389

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51

<210> 2390

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2389 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39565239

<400> 2390
tcaagggacc cgaagactag gggaggagca gcgagcgggt cgcggccgcc t 51

<210> 2391
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2392 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39571018

<400> 2391
cctctggtcc cggtgctaag agcagggttg gtctgcagc ttcttggtg c 51

<210> 2392
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2391 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39571018

<400> 2392
cctctggtcc cggtgctaag agcagagttg gtctgcagc ttcttggtg c 51

<210> 2393
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2394 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39571022

<400> 2393
ctgcatccgc tggtggcaga gacacagttg ggggaggcag aggtggcact g 51

<210> 2394
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2393 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39571022

<400> 2394

ctgcatccgc tgggtggcaga gacacggttg ggggaggcag aggtggcact g

51

<210> 2395

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2396 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39574041

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51

<210> 2396

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2395 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39574041

<400> 2396

tttgggaggc cgaggcgggc ggatggcaag atcaggagtt tgagaccagc c

51

<210> 2397

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2398 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39574041

<400> 2397
tgggaggccg aggcgggcgg atgacaagat caggagttag agaccagcct g 51

<210> 2398
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2397 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39574041

<400> 2398
tgggaggccg aggcgggcgg atgacgagat caggagttag agaccagcct g 51

<210> 2399
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2400 is other entry)

<221> misc_feature
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<223> Accession number cg39575681

<400> 2399
gcattgggtc tgccccgata gtcggggcgt aggggtgcca gacatgacgt c 51

<210> 2400
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2399 is other entry)

<221> misc_feature
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<223> Accession number cg39575681

<400> 2400

gcattggggtc tgccccgatc gtcggtgctg aggggtgccca gacatgacgt c

51

<210> 2401

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2402 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39575791

<400> 2401

agcacacaaa tgcccacgta tgtgcatgca tgaaaacaca tgaaacacac a

51

<210> 2402

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2401 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39575791

<400> 2402

agcacacaaa tgcccacgta tgtgcgtgca tgaaaacaca tgaaacacac a

51

<210> 2403

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2404 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39575791

<400> 2403

gcacacgtgc acacacacag ccacatgcac acatccacac gcacgcacac a

51

<210> 2404

<211> 51

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2403 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39575791

<400> 2404
gcacacgtgc acacacacag ccacacgcac acatccacac gcacgcacac a 51

<210> 2405
<211> 45
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2406 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39575852

<400> 2405
gatgcggacc tcagtggcct gcaggcgagc cggaagcca gcggt 45

<210> 2406
<211> 44
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2405 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39575852

<400> 2406
gatgcggacc tcagtggcct gcagggcagc gggaagccac gcgt 44

<210> 2407
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2408 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39575854

<400> 2407
gacgccgcga cttccggaag attctcgggg ttcgtgtagc taccagggc g . 51

<210> 2408
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2407 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39575854

<400> 2408
gacgccgcga cttccggaag attcttgggg ttcgtgtagc taccagggc g 51

<210> 2409
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2410 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39575897

<400> 2409
ctctgttaag ctctcacca gccatcttcc cagcgcttct ctccctggg c 51

<210> 2410
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2409 is other entry)

<221> misc_feature
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<223> Accession number cg39575897

<400> 2410

ctctgttaag ctctcacca gccattttcc cagcgctct ctccctggg c

51

<210> 2411

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2412 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39581994

<400> 2411

gagatcaaga ccattcctggc taacacaggg aaaaccccgct ctctattaaa a

51

<210> 2412

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2411 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39581994

<400> 2412

gagatcaaga ccattcctggc taacataggg aaaaccccgct ctctattaaa a

51

<210> 2413

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2414 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39581994

<400> 2413

ctagcctgac ctgactgtta gaggccaat cactgtaagc caccaagctg c

51

<210> 2414

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2413 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39581994

<400> 2414
ctagcctgac ctgactgtta gagtgtcaat cactgtaagc caccaagctg c 51

<210> 2415
<211> 51
<212> DNA
<213> Homo sapiens

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<221> misc_feature
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<223> Accession number cg39582114

<400> 2415
aagacgggtc ggggtgggtag ccgacgtcgc cgccgacccc gtgcgctcgc t 51

<210> 2416
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (2415 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39582114

<400> 2416
aagacgggtc ggggtgggtag ccgacatcgc cgccgacccc gtgcgctcgc t 51

<210> 2417
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2418 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39582195

<400> 2417
gttcactgtg aaagcattct gcacccccac aactccgcct ctggcctggc c 51

<210> 2418
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2417 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39582195

<400> 2418
gttcactgtg aaagcattct gcacctccac aactccgcct ctggcctggc c 51

<210> 2419
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2420 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39584802

<400> 2419
atctaacgag ctcagccggc agctgcacgt gggaccagcc ctctgagctt c 51

<210> 2420
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2419 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
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<400> 2420
atctaacgag ctcagccggc agctgacgtg ggaccagccc tctgagcttc 50

<210> 2421
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2422 is other entry)

<221> misc_feature
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<223> Accession number cg39584802

<400> 2421
gaaaccaata cgaagataaa atgggaaaaa aaaaatccca ttcacggcac a 51

<210> 2422
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2421 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39584802

<400> 2422
gaaaccaata cgaagataaa atgggaaaaa aaaatcccat tcacggcaca 50

<210> 2423
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2424 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg39584802

<400> 2423
acgaagataa aatgggaaaa aaaaaatccc attcacggca cagcctgccg a 51

<210> 2424
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2423 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg39584802

<400> 2424
acgaagataa aatgggaaaa aaaaaatccca ttcacggcac agcctgccga 50

<210> 2425
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (2426 is other entry)

<221> misc_feature
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<223> Accession number cg39585484

<400> 2425
agacatggac ccacacacaa acatatgtgg acacacatgt acaaacatgc a 51

<210> 2426
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2425 is other entry)

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<223> Accession number cg39585484

<400> 2426
agacatggac ccacacacaa acatacgtgg acacacatgt acaaacatgc a 51

<210> 2427
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2428 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39587361

<400> 2427
cacatgcata catgcccaca cacacactca tacaggtata cacacccata t 51

<210> 2428
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2427 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39587361

<400> 2428
cacatgcata catgcccaca cacacctcat acaggtatac acacccata 50

<210> 2429
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2430 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39587933

<400> 2429

acacagccag aatacagcaa atacagaggc gaatgccagc agcaaaccac t

51

<210> 2430

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> 2 of 2 allelic variants (2429 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39587933

<400> 2430

acacagccag aatacagcaa atacataggc gaatgccagc agcaaaccac t

51

<210> 2431

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2432 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39587933

<400> 2431

agccagaata cagcaaatac agaggcgaat gccagcagca aaccactgaa c

51

<210> 2432

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2431 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39587933

<400> 2432

agccagaata cagcaaatac agaggtgaat gccagcagca aaccactgaa c

51

<210> 2433

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2434 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39587933

<400> 2433
cagcagcaaa ccactgaact gagaataggt cccctattga aggaatcaga g 51

<210> 2434
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2433 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39587933

<400> 2434
cagcagcaaa ccactgaact gagaacaggt cccctattga aggaatcaga g 51

<210> 2435
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2436 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39587933

<400> 2435
agcaaaccac tgaactgaga ataggtcccc tattgaagga atcagagaaa g 51

<210> 2436
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2435 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39587933

<400> 2436
agcaaaccac tgaactgaga ataggacccc tattgaagga atcagagaaa g 51

<210> 2437
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2438 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39587933

<400> 2437
accactgaac tgagaatagg tcccctattg aaggaatcag agaaagaact g 51

<210> 2438
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2437 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39587933

<400> 2438
accactgaac tgagaatagg tccccattg aaggaatcag agaaagaact g 51

<210> 2439
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2440 is other entry)

<221> misc_feature
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<223> Accession number cg39587933

<400> 2439
cccctattga aggaatcaga gaaagaactg gaagagcttg aaggggctcg a 51

<210> 2440
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2439 is other entry)

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<222> (0)...(0)
<223> Accession number cg39587933

<400> 2440
cccctattga aggaatcaga gaaaggactg gaagagcttg aaggggctcg a 51

<210> 2441
<211> 51
<212> DNA
<213> Homo sapiens

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<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2442 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39587933

<400> 2441
tcgagacccc aaaagtacaa caatgccaaag caaccagagc ttccagggac t 51

<210> 2442
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2441 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39587933

<400> 2442
tcgagacccc aaaagtacaa caatgtcaag caaccagagc ttccagggac t 51

<210> 2443
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2444 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39587933

<400> 2443
ccaaaagtac aacaatgcca agcaaccaga gcttccaggg actaagccac t 51

<210> 2444
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2443 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39587933

<400> 2444
ccaaaagtac aacaatgcca agcaatcaga gcttccaggg actaagccac t 51

<210> 2445
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2446 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39592883

<400> 2445
ttgtcacttt tgctttcaga gtcactgctg ctgtaataat ccttgatcat g 51

<210> 2446
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2445 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg39592883

<400> 2446
ttgtcacttt tgctttcaga gtcaccgctg ctgtaataat ccttgtagat g 51

<210> 2447
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2448 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39597328

<400> 2447
ttcttcctat actacaattt tttttcattt ttttcctaat gtagcgaagc 50

<210> 2448
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2447 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39597328

<400> 2448
ttcttcctat actacaattt ttttttcatt ttttcctaa ttagcgaag c 51

<210> 2449
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2450 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39597389

<400> 2449
ttgggggact agaggagga tagcattagg agaaatacct aaaaaaagaa a 51

<210> 2450
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2449 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39597389

<400> 2450
ttgggggact agaggagga tagcactagg agaaatacct aaaaaaagaa a 51

<210> 2451
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2452 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39597389

<400> 2451
ttcccttttg agtcctgaac cccgacgtgc aaaaccatcc cttatcgatg a 51

<210> 2452
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2451 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39597389

<400> 2452
ttcccttttg agtcctgaac cccgatgtgc aaaaccatcc cttatcgatg a 51

<210> 2453
<211> 44

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2454 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39602141

<400> 2453
gagggctagt ccagccttgt acaggctccg cccttgacac cggt

44

<210> 2454
<211> 44
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2453 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39602141

<400> 2454
gagggctagt ccagccttgt acagggtccg cccttgacac cggt

44

<210> 2455
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2456 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39602254

<400> 2455
gagacagggt ttcaccatgt tgaccgggct ggtctcgaac tcctgacctc a

51

<210> 2456
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 2 of 2 allelic variants (2455 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39602254

<400> 2456

gagacagggt ttcacatgt tgaccagggt ggtctcgaac tcctgacctc a

51

<210> 2457

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2458 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39602496

<400> 2457

cctccgggtcc agacctcgcc ccagggttgc ccagagatgt aatccaggct a

51

<210> 2458

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2457 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39602496

<400> 2458

cctccgggtcc agacctcgcc ccagggttgc ccagagatgt aatccaggct a

51

<210> 2459

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2460 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39607243

<400> 2459
atgctgtgtg tgtgtgtgtg tgtgtttttt gggggatgtg ggggcctgga 50

<210> 2460
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2459 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39607243

<400> 2460
atgctgtgtg tgtgtgtgtg tgtgtgtttt tgggggatgt gggggcctgg a 51

<210> 2461
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2462 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39607243

<400> 2461
gtgtgtgtgt gtgtgtgtgt tttttggggg atgtgggggc ctggagcctg 50

<210> 2462
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2461 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg39607243

<400> 2462

gtgtgtgtgt gtgtgtgtgt ttttttgggg gatgtggggg cctggagcct g

51

<210> 2463

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2464 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39607270

<400> 2463

ccccagcggc ctggcgccca tggcagttcg gcagccgctc accgatactc g

51

<210> 2464

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2463 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39607270

<400> 2464

ccccagcggc ctggcgccca tggcaattcg gcagccgctc accgatactc g

51

<210> 2465

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2466 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39612908

<400> 2465

tctatgcagg acgccgggttc tgaagttgac agatacacca tcaatgagca a

51

<210> 2466

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2465 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39612908

<400> 2466
tctatgcagg acgccggttc tgaagctgac agatacacca tcaatgagca a 51

<210> 2467
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2468 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39612908

<400> 2467
ccggttctga agttgacaga tacaccatca atgagcaaaa ccgatttgac a 51

<210> 2468
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2467 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39612908

<400> 2468
ccggttctga agttgacaga tacacatcaa tgagcaaaac cgatttgaca 50

<210> 2469
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2470 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39660253

<400> 2469

accctccccc cccaggtcct ggcagactcg atgcacagaa ggctgtgagc g

51

<210> 2470

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2469 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39660253

<400> 2470

accctccccc cccaggtcct ggcagtcctcg atgcacagaa ggctgtgagc g

51

<210> 2471

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

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<223> Accession number cg39660253

<400> 2471

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51

<210> 2472

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<223> 2 of 2 allelic variants (2471 is other entry)

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<400> 2472
aggctcctggc agactcgatg cacagcaggc tgtgagcgga cctggctggg g 51

<210> 2473
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (2474 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39666355

<400> 2473
ttctgggatt acgcaggtgt gagccaccgt acctggccct ttttttttta t 51

<210> 2474
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2473 is other entry)

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<400> 2474
ttctgggatt acgcaggtgt gagccccgt acctggccct ttttttttta t 51

<210> 2475
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<223> 1 of 2 allelic variants (2476 is other entry)

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<400> 2475

ccaccgtacc tggccctttt tttttatattt ttaagacaag gtattgctct g 51

<210> 2476

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<223> Accession number cg39666355

<400> 2476

ccaccgtacc tggccctttt tttttatattt taagacaagg tattgctctg 50

<210> 2477

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2478 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg39667412

<400> 2477

tgtgtttcca caccgagga tgtgtggcg ggtgcatgtg caccatggcg t 51

<210> 2478

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2477 is other entry)

<221> misc_feature

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<223> Accession number cg39667412

<400> 2478

tgtgtttcca caccgagga tgtgtaggcg ggtgcatgtg caccatggcg t 51

<210> 2479
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<223> 1 of 2 allelic variants (2480 is other entry)

<221> misc_feature
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<223> Accession number cg39667412

<400> 2479
cacgtgcacc atggcgtgca cacaaggggg actgtcaatc acaggctttc a 51

<210> 2480
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<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<400> 2480
cacgtgcacc atggcgtgca cacaagggga ctgtcaatca caggctttca 50

<210> 2481
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2482 is other entry)

<221> misc_feature
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<223> Accession number cg39667412

<400> 2481
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<210> 2482
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<212> DNA

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<400> 2482

tgcacatgg cgtgcacaca aggggactgt caatcacagg ctttcatatg

50

<210> 2483

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2484 is other entry)

<221> misc_feature

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<223> Accession number cg39704218

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51

<210> 2484

<211> 51

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<223> 2 of 2 allelic variants (2483 is other entry)

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<223> Accession number cg39704218

<400> 2484

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51

<210> 2485

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2486 is other entry)

<221> misc_feature
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<223> Accession number cg39706539

<400> 2485
caagctctgc tggctactcc agtgggggtca acatttcaag aatggtacaa g 51

<210> 2486
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<223> 2 of 2 allelic variants (2485 is other entry)

<221> misc_feature
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<223> Accession number cg39706539

<400> 2486
caagctctgc tggctactcc agtgggagtca acatttcaag aatggtacaa g 51

<210> 2487
<211> 51
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<220>
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<223> 1 of 2 allelic variants (2488 is other entry)

<221> misc_feature
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<223> Accession number cg39706539

<400> 2487
ttacaagcag ctgggcttgg tggctcatgc ctataatccc agcactttaa a 51

<210> 2488
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<223> Accession number cg39706539

<400> 2488
ttacaagcag ctgggcttgg tggctgatgc ctataatccc agcactttaa a 51

<210> 2489
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (2490 is other entry)

<221> misc_feature
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<223> Accession number cg39706617

<400> 2489
catattcttc acctagcttc caaaacctat acttctcctg gcttttctct g 51

<210> 2490
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2489 is other entry)

<221> misc_feature
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<223> Accession number cg39706617

<400> 2490
catattcttc acctagcttc caaaatctat acttctcctg gcttttctct g 51

<210> 2491
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<220>
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<223> 1 of 2 allelic variants (2492 is other entry)

<221> misc_feature
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<223> Accession number cg39707457

<400> 2491
tcattaacga gggagcccg caccaggatc tggctgcctc gggtctgcag g 51

<210> 2492
<211> 51
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<223> 2 of 2 allelic variants (2491 is other entry)

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<400> 2492
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<210> 2493
<211> 51
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<220>
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<223> 1 of 2 allelic variants (2494 is other entry)

<221> misc_feature
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<400> 2493
gagcccgcca cgaggatctg gctgcctcgg ttctgcaggc tgtcgccact c 51

<210> 2494
<211> 51
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<223> 2 of 2 allelic variants (2493 is other entry)

<221> misc_feature
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<400> 2494
gagcccgcca cgaggatctg gctgcttcgg ttctgcaggc tgtcgccact c 51

<210> 2495
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (2496 is other entry)

<221> misc_feature
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<400> 2495
gctcgccgac gccgccgatg cccttaccgg tgcaaaggtg cgcgcgaccg t 51

<210> 2496
<211> 51
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<223> 2 of 2 allelic variants (2495 is other entry)

<221> misc_feature
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<400> 2496
gctcgccgac gccgccgatg cccttcccg tgcaaaggtg cgcgcgaccg t 51

<210> 2497
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (2498 is other entry)

<221> misc_feature
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<400> 2497
aggctgtcgc cactcagtgc attgccggcc tggcatgtgg tcgcccgatt c 51

<210> 2498
<211> 51
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<221> misc_feature

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<223> Accession number cg39707457

<400> 2498

aggctgtcgc cactcagtgc attgctggcc tggcatgtgg tcgcccgatt c

51

<210> 2499

<211> 51

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<223> 1 of 2 allelic variants (2500 is other entry)

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51

<210> 2501

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2502 is other entry)

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<223> Accession number cg39708746

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agccaggcat ggtggcaggt gcctgcaatc ccagctgctc gggaagctga g

51

<210> 2502
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2501 is other entry)

<221> misc_feature
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<223> Accession number cg39708746

<400> 2502
agccaggcat ggtggcaggt gcctgtaatc ccagctgctc gggaagctga g 51

<210> 2503
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2504 is other entry)

<221> misc_feature
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<223> Accession number cg39709129

<400> 2503
gttggcagcc attcatggag ggtgcctacc tgaaattggt gctcttgcc t 51

<210> 2504
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2503 is other entry)

<221> misc_feature
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<223> Accession number cg39709129

<400> 2504
gttggcagcc attcatggag ggtgcctacc tgaaattggt gctcttgcc t 51

<210> 2505
<211> 51
<212> DNA
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<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2506 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39711126

<400> 2505
gctgcctggg aactcgagcc aggggctttc tcagacttat atcagcgcta t 51

<210> 2506
<211> 50
<212> DNA
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<223> 2 of 2 allelic variants (2505 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39711126

<400> 2506
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<210> 2507
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2508 is other entry)

<221> misc_feature
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<223> Accession number cg39714236

<400> 2507
gctgaccgac actgtcccat ggtgctcact gtgtctgggc ctttggtgag a 51

<210> 2508
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (2507 is other entry)

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<223> Accession number cg39714236

<400> 2508

gctgaccgac actgtcccat ggtgccact gtgtctggtc ctttggtgag a

51

<210> 2509

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2510 is other entry)

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<223> Accession number cg39716704

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51

<210> 2510

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<212> DNA

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51

<210> 2511

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2512 is other entry)

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<223> Accession number cg39721166

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<210> 2512
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<223> 2 of 2 allelic variants (2511 is other entry)

<221> misc_feature
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<223> Accession number cg39721166

<400> 2512
tttccttatt cctaaagtat gtcctgcatt tcttgtagctg cacatctgct g 51

<210> 2513
<211> 51
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<220>
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<223> 1 of 2 allelic variants (2514 is other entry)

<221> misc_feature
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<223> Accession number cg39726191

<400> 2513
tactgaacag ccctttggaa ctctgaatga tttgggcctc acagaagctc c 51

<210> 2514
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (2513 is other entry)

<221> misc_feature
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<223> Accession number cg39726191

<400> 2514
tactgaacag ccctttggaa ctctggatga tttgggcctc acagaagctc c 51

<210> 2515
<211> 51
<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2516 is other entry)

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51

<210> 2516

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2515 is other entry)

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<223> Accession number cg39731647

<400> 2516

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51

<210> 2517

<211> 51

<212> DNA

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<221> misc_feature

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<223> Accession number cg39731647

<400> 2517

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51

<210> 2518

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2517 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg39731647

<400> 2518
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<210> 2519
<211> 51
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<223> 1 of 2 allelic variants (2520 is other entry)

<221> misc_feature
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tccacttggt ggtagcctgt ggtcttgagg ccatggaatg tccaagcctg g 51

<210> 2520
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<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2519 is other entry)

<221> misc_feature
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<223> Accession number cg39731746

<400> 2520
tccacttggt ggtagcctgt ggtctcgagg ccatggaatg tccaagcctg g 51

<210> 2521
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2522 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg39736402

<400> 2521
gccagctggc ctctgcgggc acggggcctt gccagtgca tccagcttcc a 51

<210> 2522
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<212> DNA
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<223> 2 of 2 allelic variants (2521 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg39736402

<400> 2522
gccagctggc ctctgcgggc acgggccttg cccagtgcat ccagcttcca 50

<210> 2523
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<212> DNA
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<223> 1 of 2 allelic variants (2524 is other entry)

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<223> Accession number cg39736402

<400> 2523
tggcctctgc gggcacgggg ccttgcccag tgcattccag ttccaacggg a 51

<210> 2524
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tggcctctgc gggcacgggg ccttgccagt gcatccagct toccaacggga

50

<210> 2525
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gcctctgcgg gcacggggcc ttgccagtg catccagctt ccaacgggac t

51

<210> 2526
<211> 50
<212> DNA
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<223> 2 of 2 allelic variants (2525 is other entry)

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<221> misc_feature
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<223> Accession number cg39736402

<400> 2526
gcctctgcgg gcacggggcc ttgccagtg atccagcttc caacgggact

50

<210> 2527
<211> 51
<212> DNA
<213> Homo sapiens

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<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2528 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg39736402

<400> 2527
ttccaacggg actagtccag cgccagccct gctgcccga gcacggaatc t 51

<210> 2528
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2527 is other entry)

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<223> Accession number cg39736402

<400> 2528
ttccaacggg actagtccag cgccaccctg cctgcccga cacggaatct 50

<210> 2529
<211> 51
<212> DNA
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<400> 2529
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<210> 2530
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<223> 2 of 2 allelic variants (2529 is other entry)

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<223> Accession number cg39736402

<400> 2530
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<210> 2531
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<223> 1 of 2 allelic variants (2532 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg40048937

<400> 2531
aacacaaaca cctggaaaat catggttttt ttttaaaggg gcaaagaaag 50

<210> 2532
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2531 is other entry)

<221> misc_feature
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<223> Accession number cg40048937

<400> 2532
aacacaaaca cctggaaaat catggttttt ttttaaaggg ggcaaagaaa g 51

<210> 2533
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2534 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40048937

<400> 2533

acacctggaa aatcatgggt ttttttaaag ggggcaaaga aagacatttc a

51

<210> 2534

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2533 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg40048937

<400> 2534

acacctggaa aatcatgggt ttttttaaag ggggcaaaga agacatttca

50

<210> 2535

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> 1 of 2 allelic variants (2536 is other entry)

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<222> (0)...(0)

<223> Accession number cg40048937

<400> 2535

ggtattacat ttagaaattg gaattctaca tttcaagcag aacacctgtg a

51

<210> 2536

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2535 is other entry)

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<222> (0)...(0)

<223> Accession number cg40048937

<400> 2536

ggtattacat ttagaaattg gaattttaca tttcaagcag aacacctgtg a

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<210> 2537

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2538 is other entry)

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<222> (0)...(0)

<223> Accession number cg40088791

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cggggctccg taaggcacag ccgagaggga ggtggggagg cccagtcg a

51

<210> 2538

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2537 is other entry)

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<223> Accession number cg40088791

<400> 2538

cggggctccg taaggcacag ccgaggggga ggtggggagg cccagtcg a

51

<210> 2539

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2540 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg40088791

<400> 2539

atcccagcta ctcaggaggc tgaggtggga ggatcacttg aaccccagga g

51

<210> 2540

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2539 is other entry)

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<223> Accession number cg40088791

<400> 2540
atcccagcta ctcaggaggc tgaggcggga ggatcacttg aaccccagga g 51

<210> 2541
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<223> 1 of 2 allelic variants (2542 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40154721

<400> 2541
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<210> 2542
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2541 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40154721

<400> 2542
acagtga gcc aagattgtgc cactgtactc cagcctgggc gacagagtga g 51

<210> 2543
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (2544 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg40274847

<400> 2543

taaggctgga aaggaggagc tagatcggag gagaaacatc agcaggactt g

51

<210> 2544

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (2543 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg40274847

<400> 2544

taaggctgga aaggaggagc tagattggag gagaaacatc agcaggactt g

51

<210> 2545

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> 1 of 2 allelic variants (2546 is other entry)

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<223> Accession number cg40274847

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51

<210> 2546

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2545 is other entry)

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<223> Accession number cg40274847

<400> 2546

acgttgccca ggctggtctc aaacacctgg ctcaaacaat cctcccatct t

51

<210> 2547

<211> 51
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2548 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40296356

<400> 2547
agttctcccc aagggatggc aacgcacctg tgtgccgggc tccgcgcaag g 51

<210> 2548
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (2547 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40296356

<400> 2548
agttctcccc aagggatggc aacgcgcttg tgtgccgggc tccgcgcaag g 51

<210> 2549
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2550 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40296356

<400> 2549
gatggcaacg cacctgtgtg ccgggctccg cgcaagggtt ttccctgttt a 51

<210> 2550
<211> 50
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (2549 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40296356

<400> 2550
gatggcaacg cacctgtgtg ccgggtccgc gcaagggctt tccctgttta 50

<210> 2551
<211> 51
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<213> Homo sapiens

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<223> 1 of 2 allelic variants (2552 is other entry)

<221> misc_feature
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<223> Accession number cg40303588

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ccttgattat gtgagtaatg cgagtacctg gttgtttcag ttgaaggtgc t 51

<210> 2552
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (2551 is other entry)

<221> misc_feature
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<223> Accession number cg40303588

<400> 2552
ccttgattat gtgagtaatg cgagtgccctg gttgtttcag ttgaaggtgc t 51

<210> 2553
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2554 is other entry)

<221> misc_feature
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<223> Accession number cg40303588

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agttgaaggt gctgtattga cttgcccttt tcattcctct ccatgagagc c 51

<210> 2554
<211> 51
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<223> 2 of 2 allelic variants (2553 is other entry)

<221> misc_feature
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<223> Accession number cg40303588

<400> 2554
agttgaaggt gctgtattga cttgctcttt tcattcctct ccatgagagc c 51

<210> 2555
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<223> 1 of 2 allelic variants (2556 is other entry)

<221> misc_feature
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<223> Accession number cg40307796

<400> 2555
gcaggagaag acctccttgt tcccatggct catggccaag ttgctcccat c 51

<210> 2556
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2555 is other entry)

<221> misc_feature
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<400> 2556

gcaggagaag acctccttgt tcccacggct catggccacg ttgctcccat c

51

<210> 2557

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2558 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg40307796

<400> 2557

cactggtctc aggtcgctgc cctccttttc ctcttctggg agtggaggct c

51

<210> 2558

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2557 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg40307796

<400> 2558

cactggtctc aggtcgctgc cctccatttc ctcttctggg agtggaggct c

51

<210> 2559

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2560 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg40312834

<400> 2559

aatcttgggc acccgtttct cgcaggaat ggcaggagat ccaggaagg g

51

<210> 2560

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2559 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40312834

<400> 2560
aatcttgggc acccgtttct ccgcagaatg gcaggagatc cagggaaggg 50

<210> 2561
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (2562 is other entry).

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40329454

<400> 2561
cgcacgcggtt ggccggggcg cgcggtgctt ggctgcggtg ctcacactca t 51

<210> 2562
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2561 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40329454

<400> 2562
cgcacgcggtt ggccggggcg cgcggggctt ggctgcggtg ctcacactca t 51

<210> 2563
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<223> 1 of 2 allelic variants (2564 is other entry)

<221> misc_feature
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<223> Accession number cg40341796

<400> 2563
taacataagc agtgaaaatg agacaatgga gtatgggaag caaaaaataa g 51

<210> 2564
<211> 51
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<223> 2 of 2 allelic variants (2563 is other entry)

<221> misc_feature
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<223> Accession number cg40341796

<400> 2564
taacataagc agtgaaaatg agacagtgga gtatgggaag caaaaaataa g 51

<210> 2565
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (2566 is other entry)

<221> misc_feature
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<223> Accession number cg40341796

<400> 2565
tgaaaatgag acaatggagt atgggaagca aaaaataagt cattaggcag a 51

<210> 2566
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (2565 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg40341796

<400> 2566

tgaaaatgag acaatggagt atggggagca aaaaataagt cattaggcag a

51

<210> 2567

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2568 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg40381397

<400> 2567

cttgtagttg ctggtacaa acctggcct ccacaatggc aatgggggag t

51

<210> 2568

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2567 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg40381397

<400> 2568

cttgtagttg ctggtacaa acctgtgcct ccacaatggc aatgggggag t

51

<210> 2569

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2570 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg40385017

<400> 2569

aaaacttaaa gtataataaa aaaaaattta tattaaatta atctgtatgt g

51

<210> 2570

<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2569 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40385017

<400> 2570
aaaacttaaa gtataataaa aaaaatttat attaaattaa tctgtatgtg

50

<210> 2571
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2572 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40389166

<400> 2571
tgctgggacc acaggcgtga gcccctgcac ccggcctgat ttacatcatt t

51

<210> 2572
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2571 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40389166

<400> 2572
tgctgggacc acaggcgtga gccccgcac ccggcctgat ttacatcatt t

51

<210> 2573
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2574 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg40389419

<400> 2573

aaggttcaaa gtttcaataa atcccggaaa actacattcc taaaggctgt g

51

<210> 2574

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2573 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg40389419

<400> 2574

aaggttcaaa gtttcaataa atcccagaaa actacattcc taaaggctgt g

51

<210> 2575

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

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<223> 1 of 2 allelic variants (2576 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg40790872

<400> 2575

tctactaaaa atacaaaaat tagccaggca tgggtggcagg cacctgtagt c

51

<210> 2576

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2575 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40790872

<400> 2576
tctactaaaa atacaaaaat tagccgggca tgggtggcagg cacctgtagt c 51

<210> 2577
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2578 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40790872

<400> 2577
aaattagcca ggcattggtgg caggcacctg tagtcccagc tactcgggag g 51

<210> 2578
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2577 is other entry)

<221> misc_feature
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<223> Accession number cg40790872

<400> 2578
aaattagcca ggcattggtgg caggcgctg tagtcccagc tactcgggag g 51

<210> 2579
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<212> DNA
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<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2580 is other entry)

<221> misc_feature
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<400> 2579

tccggccgtg ggcgccagaa gcggtgtgt aaatatgtgt gaacaagcgc t

51

<210> 2580

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2579 is other entry)

<221> misc_feature

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<223> Accession number cg40797606

<400> 2580

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51

<210> 2581

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2582 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg40797606

<400> 2581

acatgcttta agacttgact tcggggaaaa aaaaaaaaaa aaattttttt t

51

<210> 2582

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

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<221> misc_feature

<222> (0)...(0)

<223> Accession number cg40797606

<400> 2582

acatgcttta agacttgact tcggggaaaa aaaaaaaaaa aaattttttt t

51

<210> 2583

<211> 51

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2584 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40885230

<400> 2583
cctgggcctc cagctgctgc agaaggatgc cgccgccgcc cctgccaccc c 51

<210> 2584
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2583 is other entry)

<221> misc_feature
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<223> Accession number cg40885230

<400> 2584
cctgggcctc cagctgctgc agaagaatgc cgccgccgcc cctgccaccc c 51

<210> 2585
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2586 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40927039

<400> 2585
gcgttcttcg gcatcttctt tggggccctg ggcggcctct tgctgctggg g 51

<210> 2586
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2585 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40927039

<400> 2586
gcgttcttcg gcattcttctt tggggctcctg ggcggcctct tgctgctggg g 51

<210> 2587
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2588 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40932131

<400> 2587
tgaaagaagc ttttaacacc tgaaagtcac ctcaaaatgg atatatgggt a 51

<210> 2588
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2587 is other entry)

<221> misc_feature
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<223> Accession number cg40932131

<400> 2588
tgaaagaagc ttttaacacc tgaaaatcat ctcaaaatgg atatatgggt a 51

<210> 2589
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2590 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40949022

<400> 2589
tcagagacca gcccgcccaa catggcgaaa ccccgctctcc actaaaaata c 51

<210> 2590
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2589 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40949022

<400> 2590
tcagagacca gcccgccaa catggtgaaa ccccgctctcc actaaaaata c 51

<210> 2591
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2592 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40949022

<400> 2591
cagcccggcc aacatggcga aaccccgctct ccactaaaaa tacaaaaaat c 51

<210> 2592
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> 2 of 2 allelic variants (2591 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40949022

<400> 2592
cagcccggcc aacatggcga aaccctgtct ccactaaaaa tacaaaaaat c 51

<210> 2593
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2594 is other entry)

<221> misc_feature
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<223> Accession number cg40949022

<400> 2593
ggccaacatg gcgaaacccc gtctccacta aaaatacaaaa aaatcagcca g 51

<210> 2594
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2593 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40949022

<400> 2594
ggccaacatg gcgaaacccc gtctctacta aaaatacaaaa aaatcagcca g 51

<210> 2595
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2596 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40987225

<400> 2595
caacatggca aaaccccatc tctacaaaaa atacaaaaag attagccagg c 51

<210> 2596
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2595 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg40987225

<400> 2596
caacatggca aaaccccatc tctactaaaa atacaaaaag attagccagg c 51

<210> 2597
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2598 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40999240

<400> 2597
ttcgccatgt tggccaggct ggtcttgacc tcttgagctc aagagatcca c 51

<210> 2598
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2597 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg40999240

<400> 2598
ttcgccatgt tggccaggct ggtctcgacc tcttgagctc aagagatcca c 51

<210> 2599
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2600 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg41038983

<400> 2599
cgcttccccg ctcagcgcac tcagtttgcg gctgggaatg accctcgccg c 51

<210> 2600

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2599 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg41038983

<400> 2600

cgcttccccg ctcagegcac tcagtctgcg gctgggaatg accctcgccg c

51

<210> 2601

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2602 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg41060726

<400> 2601

caatgggcaa atacacattt tcttggtatt ctccacaaga ataaactaat a

51

<210> 2602

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2601 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg41060726

<400> 2602

caatgggcaa atacacattt tcttgatatt ctccacaaga ataaactaat a

51

<210> 2603

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2604 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg41060726

<400> 2603
catctcttac cctctaaaaa aaaaaaggca attatttttaa ttccctgtaa t 51

<210> 2604
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2603 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg41060726

<400> 2604
catctcttac cctctaaaaa aaaaaggcaa ttatttttaat tccttgtaat 50

<210> 2605
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2606 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg41066315

<400> 2605
aggccgcttt ccccttcttc tcgccctgcg gcagagagcg caacttctg c 51

<210> 2606
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 2 of 2 allelic variants (2605 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg41066315

<400> 2606

aggccgcttt ccccttcttc tcgcctgcgg cagagagcgc aacttctctg

50

<210> 2607

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2608 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg41066315

<400> 2607

ctcctactgc ggcggtggcg aggcctggc cgtgcccttc gagccggcgc g

51

<210> 2608

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2607 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg41066315

<400> 2608

ctcctactgc ggcggtggcg aggcctggcc gtgcccttcg agccggcgcg

50

<210> 2609

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
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<223> 1 of 2 allelic variants (2610 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg41066315

<400> 2609
actgcggcgg tggcgaggcc ctggccgtgc ccttcgagcc ggcgcgcctg c 51

<210> 2610
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2609 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg41066315

<400> 2610
actgcggcgg tggcgaggcc ctggcgtgcc cttcgagccg ggcgcgcctgc 50

<210> 2611
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2612 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg41079413

<400> 2611
cctcttcccg ccttttccga gacttcctta gacctcatga tgtctggaat g 51

<210> 2612
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)

<223> 2 of 2 allelic variants (2611 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg41079413

<400> 2612

cctcttcccg ccttttccga gactttctta gacctcatga tgtctggaat g

51

<210> 2613

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2614 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg41079413

<400> 2613

cttagacctc atgatgtctg gaatgtgacc tgggagatgc tgcagcctcc a

51

<210> 2614

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2613 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg41079413

<400> 2614

cttagacctc atgatgtctg gaatgggacc tgggagatgc tgcagcctcc a

51

<210> 2615

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2616 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg41084544

<400> 2615
acaggcatgc accaccatgc ccggctaatt ttgtattttt agtggagacg g 51

<210> 2616
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2615 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg41084544

<400> 2616
acaggcatgc accaccatgc ccggccaatt ttgtattttt agtggagacg g 51

<210> 2617
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2618 is other entry)

<221> misc_feature
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<223> Accession number cg41084544

<400> 2617
tcgaactccc aacgtcaggt gatccgctg cctaggcctc ccaaagtgt g 51

<210> 2618
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2617 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg41084544

<400> 2618
tcgaactccc aacgtcaggt gatccacctg cctaggcctc ccaaagtgt g 51

<210> 2619
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2620 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg41084998

<400> 2619

ggagctggga gtatccctca aagccagggc ctgggatggg cattagcttg t

51

<210> 2620

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2619 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg41084998

<400> 2620

ggagctggga gtatccctca aagccggggc ctgggatggg cattagcttg t

51

<210> 2621

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2622 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg41085370

<400> 2621

aaggctctta aagcaacatt taaacttttt ggcggtgtc atttctgtga g

51

<210> 2622

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2621 is other entry)